21-SEP-2000

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The present sequence represents a human platelet-derived growth factor C (PDGF-C) (formally designated VEGF-F) fragment. PDGF-C polypeptides have the ability to stimulate and enhance proliferation or differentiation, and/or growth or motility of cells expressing a PDGF-C receptor.

C PDGF-C polypeptides can be used in pharmaceuticals for promoting cell proliferation, preferably in combination with one other growth factor and heparin. Pharmaceuticals comprising PDGF-C polypeptides can also be used for stimulating connective tissue or wound healing. The C PDGF-C polypeptide can be enzymatically processed to generate the active truncated form of PDGF-C and used to regulate the receptor inding specificity of PDGF-C. PDGF-C and also be used to promote fibroblast mitogenesis in a mammal and to induce PDGF alpha receptor activation.

C Antagonists can be used to inhibit tumour growth of a tumour expressing PDGF-C in a mammal. Specific types of human tumours, e.g. choriocarcinoma, Wilms tumour, megakaryoblastic leukeamia, lung carcinoma and erythroleukemia, can be dentified by testing for expression of PDGF-C. PDGF-C antagonists can also be used to inhibit tissue remodelling during invasion of tumour cells into a normal population of cells. Antagonists can also be used to inhibit conditions,
                                                                                                                                                                                                                     Novel DNA encoding PDGF-C useful to stimulate or enhance proliferation, differentiation, growth and motility of cells expressing the PDGF-C \,
                                                                                   Uutela M, Alitalo K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               especially found in the lung, kidney or liver.
                                                                                   Ponten A,
                (LUDW-) LUDWIG INST CANCER RES. (UYHE-) UNIV HELSINKI LICENSING LTD.
                                                                                   Lee X, Pont
Betsholz C;
                                                                                                                                                                                                                                                                                                           Disclosure; Fig 4; 135pp; English.
                                                                                   Aase K,
Heldin C,
                                                                                                                                                  2000-292954/25
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                                                                                                                                                                       N-PSDB; AAA12524
                                                                                 Eriksson U,
                                                                                                          Oestman A,
                                                                                                                                                                                                                   Novel DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                 receptor
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Gaps 1 AFVFGRKSRVVDLNLLTEEVRLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGGNCA 60 ; Length 318; Indels Score 666; DB 21; I Pred. No. 5e-62; 100.0%; Sc 100.0%; Pr tive 0; Matches 120; Conservative Similarity Query Match Best Local δŏ

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61 CCLHNCNECQCVPSKVTKKYHEVLQLRPKTGVRGLHKSLTDVALEHHEECDCVCRGSTGG 120 259 g δ g

AAB58438 standard; Protein; 339 AA AAB58438; RESULT AAB58438 

(first entry) 14-MAR-2001

Lung cancer associated polypeptide sequence SEQ ID 776.

cardioactive; immunomodulatory; muscular active; vulnerary; gastrointestinal; nephrotropic; antiinfective; gynecological; antibacterial; diagnosis; neural disorder; immune disorder; reproductive; proliferative disorder; wound healing; infectious disease. Human; lung cancer associated protein; neuroprotective; cytostatic;

Homo sapiens

WO200055180-A2

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Polynucleotide sequences AAF17982 - AAF18424 encode human lung cancer associated proteins represented in AAB58106 - AAB58548. Lung cancer associated proteins and polynucleotide sequences, their agonists, and antagonists may have neuroprotective; cytostatic; cardioactive; cardioactive; cardioactive; cardioactive; cardioactive; immunomodulatory; muscular active general; vulnerary; gastrointestinal general; nephrotropic; antilnfective; gynecological; or antibacterial activity. The invention also includes antibodies specific for the protein or polynucleotide sequences. The lung cancer associated polynucleotide sequences. The lung cancer associated chromosome identification, as chromosome markers, and fung cancer, chromosome identification, as chromosome markers, and for numerous other diagnostic or research purposes. The proteins may be used to treat disorders such as neural, immune, muscular, reproductive, gastrointestinal, pulmonary, cardiovascular, reproductive, disorders. The proteins may also be used in the treatment of wounds and confident and proliferative disorders. The proteins may also be used in the treatment of wounds and cancer and dispesses. Polynucleotide sequences AAP1845 - AAB18433 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lung cancer associated gene sequences, referred to as lung cancer antigens, useful for treatment, prevention, and diagnosis of disorders such as lung cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           peptide AAB58549 are used in the course of the invention for the identification and characterisation of the polynucleotide and protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 11; Page 1305-1306; 1425pp; English.
                                                                                                                                                                                                                        (HUMA-) HUMAN GENOME SCI INC
08-MAR-2000; 2000WO-US05918
                                                                                                            99US-0124270.
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                                                                                                                                                                                                                                                                           (ROSE/) ROSEN C A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; AAF18314
                                                                                                            12-MAR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                             Ruben SM;
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Gaps 0; Length 339; Indels ; Score 666; DB 21; ; Pred. No. 5.4e-62; 0; Mismatches 0; 100.0%; Query Match 100. Best Local Similarity 100. Matches 120; Conservative

339 AA;

Seguence

0

220 afvfgrksrvvdlnllteevrlysctprnfsvsireelkrtdtifwpgcllvkrcggnca 279 9 1 AFVFGRKSRVVDLNLLTEEVRLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGGNCA δy В

CCLHNCNECOCVPSKVTKKYHEVLQLRPKTGVRGLHKSLTDVALEHHEECDCVCRGSTGG 120 61 280 ò g

AAY33679 standard; Protein; 345 AA (first entry) Human VEGF-E protein. 11-JAN-2000 AAY33679; AAY33679 

RESULT

VEGF-E; human; vascular endothelial cell growth factor; wound repair; treatment; cardiovascular disorder; endothelial disorder; therapy; tissue generation; regeneration; cardiac hypertrophy; cancer; detection; angiogenic disorder; age-related macular degeneration; vascular disease; neovascularization; tumor; gene mapping.

Homo sapiens.

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Human, PRO; EST; expressed sequence tag; PCR primer; hybridisation; probe; blood coagulation disorder; cancer; cellular adhesion disorder; secreted protein; transmembrane protein.
Human PRO200 protein sequence.
                                                                                                                                                                                                                                                                                                                                                  99WO-US05028
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98US-0081229
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98US-0083742
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27-MAR-1998;
27-MAR-1998;
27-MAR-1998;
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31-MAR-1998;
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01-APR-1998;
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27-MAR-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This invention describes the isolation of a novel human vascular endothelial cell growth factor-E (VEGF-E) polypeptide which has tranquillizer, vulnery and cardiant activity. VEGF-E can be administered therapeutically, especially by expressing encoding polynucleotides, to treat cardiovascular or endothelial disorders in mammals, especially humans it is useful in wound repair and tissue generation and cardiac hypertrophy cran be combined with a carrier in pharmaceutical compositions, which regeneration, and may especially be used to treat cardiac hypertrophy can be combined with a carrier in pharmaceutical compositions, which can be administered to treat disorders as above. VEGF-E can be used to screen for antagonists and disorders, and the antagonists administered to screen for antagonists and agonists, as above. VEGF-E can be used to despend the antagonists, as above. The antibodies, useful therapeutically as antagonists, as above. The antibodies are also useful to detect VEGF-E polypeptide, especially to diagnose cardiovascular, endothelial or angiogenic disorders in mammals (e.g. vascular disease, or neovascularization associated with tumor formation), by contacting the antibody with a tissue sample and detecting formation of an in mammals, by detecting abnormally high or low VEGF-E gene expression in the VEGF-E can be used to diagnose a disease or susceptibility to a disease related to a mutated form of VEGF-E (e.g. a cardiovascular, endothelial or anglogenic disorder such as a tumor), by cannot many also be used to adaptopenic disorder such as a tumor), by cannot be maded to the many also be used to diagnose a disease or a cardiovascular, the dothelial or anglogenic disorder such as a tumor), by cannot be maded to the many also be used to diagnose a disease or and cardiovascular, the dothelial or anglogenic disorder such as a tumor), by cannot be used to an autated form of vector and the cardiovascular, the detecting a mutated form of a disease related to a mutated form of a disease related to a mutated fo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sample. They may also be used to produce probes useful to detect related sequences or for gene mapping. This sequence represents the human VEGF-E protein described in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 CCLHNCNECQCVPSKVTKKYHEVLQLRPKTGVRGLHKSLTDVALEHHEECDCVCRGSTGG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        New growth factor polypeptide useful for treating cardiovascular or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      endothelial disorders, e.g. cardiac hypertrophy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Fig 2; 122pp; English.
                                                                                                            99WO-US05190
                                                                                                                                                                 98US-0040220.
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                                                                                                                                                                                                                                                         (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                      WPI; 1999-580306/49.
                                                                                                                                                                                                                                                                                                                 Ferrara N, Kuo SS;
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                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; AAZ23691
W09947677-A2
                                                                                                            10-MAR-1999;
                                                                                                                                                                 17-MAR-1998;
                                                                                                                                                                                                  02-NOV-1998;
                                                       23-SEP-1999.
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Sequence

Query Match

qq οy AAY41766;

AAY41766 ID AAY43

(first entry)

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Vascular endothelial growth factor related protein; VEGF-R protein; tissue growth inhibition; tumour growth; cancer; tissue growth; angiogenesis; coronary artery blockage.
                                                                                                                                                                                                                                                                                                                                       A vascular endothelial growth factor related protein and related polynucleotide, useful for identifying antagonists and binding
                                                               Human vascular endothelial growth factor related protein.
                                                                                                                                                                                                                                                                                                                                                                                Claim 1; Page 56-58; 62pp; English.
  AAY30023 standard; Protein; 345 AA
                                                                                                                                                                                                                                                                                                        WPI; 1999-458680/38.
                                                                                                                                                                                                                                                                                                                   N-PSDB; AAX86352
                                                                                                                                                                                                                                                               (ELIL ) LILLY
                                                                                                                             Homo sapiens.
                                                                                                                                               W09937671-A1
                                                                                                                                                                                       26-JAN-1999;
                                                                                                                                                                                                                                05-JUN-1998;
24-JUN-1998;
                                          11-0CT-1999
                                                                                                                                                                                                             31-AUG-1998;
27-JAN-1998;
                                                                                                                                                                    29-JUL-1999
                                                                                                                                                                                                                                                                                                                                                            compounds
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention describes secreted and transmembrane polypeptides and their polynucleotides. The nucleotide sequences are useful as sources of probes, primers, for chromosome mapping, and for generation of antisense sequences. They can also be used to create transgenic animals. The proteins can be used to treat a variety of diseases and disorders, depending on their function. Diseases that may be treated include blood coagulation disorders, cancers and cellular adhesion disorders. They may also be used to raise antibodies. AAZ33891 to AAZ34338, and AAY41685 to AAY41774 represent polynucleotide and polypeptide sequence given in the exemplification of the present
                                                                                                                                                                                                                                                                                                                                                                                       secreted and transmembrane polypeptides and their polynucleotides, in for treating blood coagulation disorders, cancers and cellular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 345;
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100.0%; Pred. No. 5.5e-62;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                       Baker
                                                                                                                                                                                                                                                                                                                                       Yuan J,
                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 12; Fig 207; 530pp; English.
                                                                                                                                                                                                                                                                                                                                       Gurney A,
98US-0084441.
98US-0084598.
98US-0084627.
98US-0084637.
98US-0084639.
98US-0084643.
98US-0084643.
98US-0085338.
98US-0085338.
                                                                                                                                             98US-0085582.
98US-0085689.
98US-0085697.
98US-0085700.
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98US-0087208
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98US-0100038
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   120; Conservative
                                                                                                                                                                                                                                                                                                              (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                      Goddard A,
                                                                                                                                                                                                                                                                                                                                                         WPI; 1999-551358/46.
N-PSDB; AAZ34296.
                                                                                                                                                                                                                                                                                                                                                                                                            adhesion disorders
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                                                                                                                                                                            15-MAY-1998;
                                                                                                                           MAY-1998;
                                                                                                                                                                                                             22-MAY-1998;
                                                                                                                                                                                                                                                                                              11-SEP-1998
                                                                                                                                                                                                                                                                                                                                      Wood WI,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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98US-0098548. 98US-0072635. 98US-0088089. 98US-0090544.

Song HY; & CO ELI

Na S,

99WO-US01574

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61 CCLHNCNECQCVPSKVTKKYHEVLQLRPKTGVRGLHKSLTDVALEHHEECDCVCRGSTGG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cclhncnecqcvpskvtkkyhevlq1rpktgvrglhksltdvalehheecdcvcrgstgg 345
The present sequence represents a vascular endothelial growth factor related (VEGF-R) protein. VEGF-R can be used in assays to identify compounds that bind to it or that antagonize its activity. VEGF-R antagonists (e.g. anti-VEGF-R antibodies) are useful for inhibiting tissue growth. This is useful for inhibiting transulate tissue aromer. VEGF-R itself can be used to stimulate tissue yerowth, anglogenesis and to treat coronary artery blockage. The VEGF-R coding sequence can be used for the recombinant production of
                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                   1 AFVFGRKSRVVDLNLLTEEVRLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGGNCA
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                                                                                                                                                                                                                                                                                                                         0; Mismatches
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                                                                                                                                                                                                                                                                                                                            Conservative
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                                                                                                                                                                          the VEGF-R protein.
                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                   345 AA;
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226 61

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1 AFVFGRKSRVVDLNLLTEEVRLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGGNCA

9

CCLHNCNECQCVPSKVTKKYHEVLQLRPKTGVRGLHKSLTDVALEHHEECDCVCRGSTGG 120

S

RESULT AAY30023

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61 CCLHNCNECQCVPSKVTKKYHEVLQLRPKTGVRGLHKSLTDVALEHHEECDCVCRGSTGG 120 

286

g

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vulnerary;

Human; platelet derived growth factor related protein; LP8; VEGFh; vascular endothelial growth factor h; tissue regeneration; vulnerar atherosclerosis; PDGF-related protein; antiarteriosclerotic.

24-MAR-2000; 2000WO-US06427.

WO200059940-A2 Homo sapiens.

12-OCT-2000

99US-0127913

06-APR-1999;

(ELIL ) LILLY & CO ELI

Na S;

Hammond LJ,

WPI; 2000-664991/64.

N-PSDB; AAC64426.

Human platelet-derived growth factor related protein LP8

(first entry)

08-FEB-2001

AAB24250;

AAB24250 standard; Protein; 345 AA

AAB24250

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The invention relates to the human growth factor homologue zvegf4

(AAB48653), and nucleic acids encoding it (AAC8155). Zvegf4 is a member
of the PDGF (platelet-derived growth factor)/VEGF (vascular endothelial)
growth factor) family. Zvegf4 has a growth factor domain (AAB48654)
characterised by a PDGF cystine knot structure, and a CUB domain
characterised by a PDGF cystine knot structure. Zvegf4 has PDGF-like
activity having mitogenic activity on fibroblasts, vascular smooth
muscle cells and pericytes, and has also been shown to stimulate bone
growth. The invention also relates to fusion proteins comprising human
cc growth. The invention also relates to fusion proteins comprising human
cc growth. The invention also relates to fusion proteins comprising human
cc growth. The invention also relates to fusion proteins comprising human
cc growth. The invention also relates to fusion proteins comprising human
cc growth. The invention also relates to fusion proteins and phuman zvegf4
nucleic acids; the recombinant expression of human zvegf4, an antibody
which binds to human zvegf4 or a fragment thereof; a method of activating
a cell-surface PDGF receptor using a zvegf4-derived polypeptide; a
cell-surface PDGF receptor using a zvegf4-derived polypeptide; a
cmethod of modulating the proliferation, differentiation, migration or
cvegf4-derived polypeptides; and a method of detecting a genetic
c abnormality in the zvegf4 gene of a patient. Zvegf4 proteins and derived
cc fragments may be used to stimulate tissue development or repair, or
ccellular differentiation or proliferation. They are particularly used for
ccellular differentiation or proper and method or development or repair, or
ccellular differentiation or proliferation. They are particularly to a
                   Human; zvegf3; zvegf4 fusion; growth factor homologue; VEGF/PDGF family; CUB domain; PDGF-like activity; mitogenic; osteogenic; neovascularisation; tissue repair; proliferation; differentiation; liver damage; neuroregenerative; Alzheimer's disease; multiple sclerosis; periodontal disease; bone fracture; wound healing; vulnerary; ischaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the treatment or repair of liver damage, and may also be used to modulate neurite growth (e.g., in the treatment of Alzheimer's disease c multiple sclerosis). Due to their osteogenic activity, they may be used in the treatment of periodontal disease and fractures. They may also be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  used to enhance expansion and mobilisation of haematopoietic stem cells and endochellal precursor stem cells, which may be useful in the treatment of ischaemia, in wound healing, and in the modulation of the immune system. The present sequence represents human zvogf3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 h factor homologs and the nucleic acids that encode them, us for treating liver damage, ischemia, multiple sclerosis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gilbertson DG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 48; Page 125-126; 143pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sheppard
                                                                                                                                                                                                                                                                                                                                                                                                                                               10-NOV-1999; 99US-0164463.
04-FEB-2000; 2000US-0180169.
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                                                                                                                                                                                                                                                                                                                                                                                                                       99US-0304216
                                                                                                                                                     immunomodulation; hepatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (ZYMO ) ZYMOGENETICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Growth factor homologs
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Alzheimer's disease -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2000-687541/67
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                                                                                                                                                                                                              Homo sapiens.
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ö Gaps 0; Length 345; Indels ; Score 666; DB 21; ; Pred. No. 5.5e-62; 0; Mismatches 0; 100.0%; 100.0%; Query Match 100. Best Local Similarity 100. Matches 120; Conservative

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61 CCLHNCNECQCVPSKVTKKYHEVLQLRPKTGVRGLHKSLTDVALEHHEECDCVCRGSTGG 120
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AAB44322
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Gaps

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0; Mismatches

Matches 120; Conservative

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Similarity

Query Match Best Local

Length 345; Indels

100.0%; Score 666; DB 21; 100.0%; Pred. No. 5.5e-62;

9

1 AFVFGRKSRVVDLNLLTEEVRLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGGNCA

the progress of atherosclerosis or treating atherosclerosis comprising the administration of an LPB antagonist. The method is useful for enhancing tissue growth, promoting wound healing and stimulating smooth muscle growth. Antagonists of LPB are useful for treating

muscle growth. Antagonists of LP8 are useful for treating atherosclerosis. The present sequence represents human LP8, which is

also called VEGFh.

345 AA;

Sednence

or

promoting wound healing or stimulating smooth muscle growth by administering a platelet-derived growth factor (PDGF) related protein, designated LP8 or its analogue. Also described is a method of slowing

The present invention describes a method for enhancing tissue growth,

Claim 4; Page 63-64; 64pp; English.

Enhancing tissue growth and promoting wound healing by administering platelet-derived growth factor related protein, LP8 or its analog and treating atherosclerosis by administering LP8 antagonist  $\,$ 

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AAC78458 to AAC78599 represent polynucleotide and EST (expressed sequence tag) sequences which encode secreted or transmembrane PRO polypeptides. The PRO polynucleotides and polypeptides have cytostatic activity. The polynucleotides and polypeptides can be used for detecting the presence of PRO polypeptides in samples, for linking bioactive molecules to cells and for modulating biological activities of cells, using the polypeptides for specific targeting. The polypeptide targeting can be used to kill the target cells, e.g. for the treatment of cancers. The polypeptide pairs provide specific targeting of bioactive molecules to cells. AAC78600 to AAC78987 represent PCR primers and probes used in
                                                                                                                                                 Human; secreted protein; transmembrane protein; PRO; EST; cytostatic; expressed sequence tag; detection; cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  o W, Gerber H, Gerritsen ME;
Gurney AL, Hillan KJ;
J, Paoni NF, Rov Wn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel PRO polypeptides and polynucleotides used in detection methods, to target bioactive molecules to specific cells, and to modulate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KP, Botstein D, Desnoyers L, Eaton E, Fong S, Gao W, Gerber H, Gerri PJ, Grimaldi CJ, Gurney AL, Hillan Napier MA, Pan J, Paoni NF, Roy M, TA, Tumas D, Williams PM, Wood WI.
                                                                                             Human PRO200 (UNQ174) protein sequence SEQ ID NO:488.
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99WO-US28313.
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99US-0126773
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99US-0145698
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2000WO-US00277
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Ferrara N, Filvaroff E,
Goddard A, Godowski PJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Stewart TA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (GETH ) GENENTECH INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2000-611443/58.
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                                                                                                                                                                                                                                                                         WO200053756-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        05-JAN-2000;
06-JAN-2000;
06-JAN-2000;
                                                                                                                                                                                                                             Homo sapiens.
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                                              08-FEB-2001
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                                                                                                                                                                                                                                                                                                                           14-SEP-2000
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16-DEC-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14-MAY-1999
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AAB44322;
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This invention describes a novel vascular endothelial growth factor-X (VEGF-X) protein (1a) and its encoding polynucleotide (IIa) which has vulnerary, cytostatic, antirheumatic, antiarthritic, antipsoriatic and antidiabetic activity and acts as an angiogenesis and vascularization regulator. An antisense molecule of the invention is useful for treating or preventing cancer, rheumatoid arthritis, psoriasis and diabetic retinopathy by inhibiting angiogenic activity or inappropriate vascularization including formation and proliferation of new blood and tissue repenir in a subject. The products of the invention and organ and tissue repenir mag abubject treating wounds such as dermal ulcers, pressure sores, venous sores, diabetic ulcers and burns and to promote
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tissue regeneration and organ repair by promoting angiogenic activity or vascularization. This sequence represents the RACE generated human VEGF-X protein described in the method of the invention.
                                                                                                                                                                                                                                                                                                                                     VEGF-X; vascular endothelial growth factor; human; vulnerary; cytostatic;
                                                                                                                                                                                                                                                                                                                                                   antirheumatic; antiarthritic; antipsoriatic; antidiabetic; treatment, anglogenesis regulator; vascularization regulator; cancer; psoriasis; rheumatoid arthritis; diabetic retinopathy; blood vessel; organ repair; tissue regeneration; tissue repair; wound; dermal ulcer; pressure sore; venous sore; diabetic ulcer; burns; skin graft growth.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New vascular endothelial growth factor protein, useful for treating or preventing diseases associated with inappropriate angiogenesis activity such as cancer, rheumatoid arthritis, psoriasis and wounds -
226 afvfgrksrvvdlnllteevrlysctprnfsvsireelkrtdtifwpgcllvkrcggnca 285
                                                                        skin graft growth, tissue repair, proliferation of new blood vessels,
                                                       61 CCLHNCNECQCVPSKVTKKYHEVLQLRPKTGVRGLHKSLTDVALEHHEECDCVCRGSTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Yon JR, Dijkmans JJH, Gosiewska A;
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Pred. No. 5.5e-62;
                                                                                                                                                                                                                                                                                                 Human RACE generated VEGF-X protein.
                                                                                                                                                                                    AAB10633 standard; Protein; 345 AA
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100.0%;
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99US-0124967.
99US-0164131.
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                                                                                                                                                                                                                                                            (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (JANC ) JANSSEN PHARM NV
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AAB10633
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0;

Indels

Length 345;

100.0%; Score 666; DB 21; 100.0%; Pred. No. 5.5e-62; Mismatches

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Conservative

al Similarity 120; Conserv

Query Match Best Local 9

Matches

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(VEGE-X) protein (Ia) and its encoding polynuclectide (IIa) which has vulnerary, cytostatic, antirheumatic, antiarthritic, antipsoriatic and antidabetic activity and acts as an angiogenesis and vasculaticand regulator. An antisense molecule of the invention is useful for treating or preventing cancer, rheumatoid arthritis, psoriasis and diabetic ethinopathy by inhibiting angiogenic activity or inappropriate vascularization including formation and proliferation of new blood vessels, growth and development of tissues, tissue regeneration and organ of the subject. The products of the invention are useful for preparing medicaments for treating wounds such as dermal ulcers, pressure sores, venous sores, diabetic ulcers and burns and to promote skin graff growth, tissue repair, proliferation of new blood vessels, tissue regeneration and organ repair by promoting angiogenic activity or vascularization. This sequence represents the human VEGF-X protein homologue described in the method of the invention.
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                                                                                                                                                                                                                                                                                                                                                                     VEGF-X; vascular endothelial growth factor; human; vulnerary; cytostatic; anticheumatic; antiarthritic; antipsoriatic; antidiabetic; treatment; anglogenesis regulator; vascularization regulator; cancer; psoriasis; rheumatoid arthritis; diabetic retinopathy; blood vessel; organ repair; tissue regeneration; tissue repair; wound; dermal ulcer; pressure sore;
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                                                     CCLHNCNECQCVPSKVTKKYHEVLQLRPKTGVRGLHKSLTDVALEHHEECDCVCRGSTGG 120
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 Gaps
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                                  1 AFVFGRKSRVVDLNLLTEEVRLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGGNCA
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Mismatches
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                                                                                                                                                                                                                                                                                                                                      Human VEGF-X homologue protein.
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99US-0164131.
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Conservative
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N-PSDB; AAA71952.
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08-NOV-1999;
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AA; 345

Sequence

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This invention describes a novel vascular endothelial growth factor-X (VEGF-X) protein (Ia) and its encoding polynucleotide (IIa) which has vulnerary, cytostatic, antirhematic, antirhentic, antipsoriatic and antidiabetic activity and acts as an angiogenesis and vascularization regulator. An antisense molecule of the invention is useful for treating concer, rheumatoid arthritis, psoriasis and diabetic retinopathy by inhibiting angiogenic activity or inappropriate vascularization including formation and proliferation of new blood vessels, growth and development of tissues, tissue regeneration and organ at tissue repair in a subject. The products of the invention are useful for preparing medicaments for treating wounds such as dermal ulcers, pressure sores, venous sores, diabetic ulcers and burns and to promote skin graft growth, tissue repair, proliferation of new blood vessels, tissue regeneration and organ repair by promoting angiogenic activity or vascularization. This sequence represents the human VEGF-X protein isolated from clones 4 and 7 described in the method of the invention.
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                                        Gaps
                                                                                          61 CCLHNCNECQCVPSKVTKKYHEVLQLRPKTGVRGLHKSLTDVALEHHEECDCVCRGSTGG
                                                                         1 AFVFGRKSRVVDLNLLTEEVRLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGGNCA
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 345;
 Length
                                      Indels
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Score 666; DB 21;
Pred. No. 5.5e-62;
Mismatches 0;
                                                                                                                                                                                                                                                                                AAB10635 standard; Protein; 345 AA
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99US-0164131.
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                                      120; Conservative
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Best Local Similarity
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08-NOV-1999;
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                                                                                                                                                                                                                                                                                                                      VEGF-X; vascular endothelial growth factor; human; vulnerary; cytostatic; antirheumatic; antiarthritic; antipsoriatic; antidiabetic; treatment; angiogenesis regulator; vascularization regulator; cancer; psoriasis; rheumatoid arthritis; diabetic retinopathy; blood vessel; organ repair; tissue regeneration; tissue regili; wound; dermal ulcer; pressure sore; venous sore; diabetic ulcer; burns; skin graft growth.
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                                                                                                                                         This invention describes a novel vascular endothelial growth factor-X
                                                                       Gaps
                                                                                              1 AFVFGRKSRVVDLNLLTEEVRLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGGNCA 60
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                                               Length 345;
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                                             Score 666; DB 21;
Pred. No. 5.5e-62;
0; Mismatches 0;
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                                             100.0%;
100.0%;
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                                             Query Match 100.
Best Local Similarity 100.
Matches 120; Conservative
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tissue regeneration and organ repair by promoting angiogenic activity or vascularization. This sequence represents the human VEGF-X protein isolated from clones 4 and 7 described in the method of the invention.
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                                                                                                                                                                                                                       Length 345;
                                                                                                                                                                                                                          Score 666; DB 21;
Pred. No. 5.5e-62;
                                                                                                                                                                                                                                                                                       0; Mismatches
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                                                                                                                                                                                                                                                              Similarity
                                                                                                                                345 AA;
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08-NOV-1999;
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                                                                                                                                   Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This invention describes a novel vascular endothelial growth factor-X (VEGF-X) protein (Ia) and its encoding polynucleotide (IIa) which has vulnerary, cytostatic, antirheumatic, antiarthritic, antipsoriatic and antidiabetic activity and acts as an angiogenesis and vascularization regulator. An antisense molecule of the invention is useful for treating or preventing cancer, rheumatoid arthritis, psoriasis and diabetic retinopathy by inhibiting angiogenic activity or inappropriate vascularization including formation and proliferation of new blood
for preparing medicaments for treating wounds such as dermal ulcers, pressure sores, venous sores, diabetic ulcers and burns and to promote skin graft growth, tissue repair, proliferation of new blood vessels, tissue regeneration and organ repair by promoting angiogenic activity or vascularization. This sequence represents a human VEGF-X protein described in the method of the invention.
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                                                                                                                                                                                                                                                                                                                     61 CCLHNCNECQCVPSKVTKKYHEVLQLRPKTGVRGLHKSLTDVALEHHEECDCVCRGSTGG 120
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                                                                                                                                                                    Length 345;
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                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sore; diabetic ulcer; burns; skin graft growth.
                                                                                                                                                                   ; DB 21;
5.5e-62;
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0
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                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                 Score 666;
Pred. No. 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Fig 11; 127pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                    AAB10650 standard; Protein; 345 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Yon JR,
                                                                                                                                                                   100.0%;
100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human 990126vegx protein.
                                                                                                                                                                                                   Matches 120; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2000-442669/38.
                                                                                                                                                                                    Best Local Similarity
                                                                                                                 345 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200037641-A2
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08-NOV-1999;
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                                                                                                                   Sequence
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                                                                                                                                                                    Query Match
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vessels, growth and development of tissues, tissue regeneration and organ and tissue repair in a subject. The products of the invention are useful for preparing medicaments for treating wounds such as dermal ulcers, pressure sores, venous sores, diabetic ulcers and burns and to promote
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VEGF-X; vascular endothelial growth factor; human; vulnerary; cytostatic; antirheumatic; antiarthritic; antipsoriatic; antidiabetic; treatment; anglogenesis regulator; vascularization regulator; cancer; psoriasis; rheumatoid arthritis; diabetic retinopathy; blood vessel; organ repair; tissue regeneration; tissue repair; wound; dermal ulcer; pressure sore; venous sore; diabetic ulcer; burns; skin graft growth.
                                                                                          or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (VEGF-X) protein (Ia) and its encoding polynucleotide (IIa) which has vulnerary, cytostatic, antirheumatic, antiarthritic, antipsoriatic and antidiabetic activity and acts as a nangiogenesis and vascularization regulator. An antisense molecule of the invention is useful for treating or preventing cancer, rheumatoid arthritis, psoriasis and diabetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           preventing diseases associated with inappropriate angiogenesis activity such as cancer, rheumatoid arthritis, psoriasis and wounds -
                                                                   skin graft growth, tissue repair, proliferation of new blood vessels, tissue regeneration and organ repair by promoting angiogenic activity o vascularization. This sequence represents the human 990126vegx protein used to illustrate the method of the invention.
                                                                                                                                                                                                                                                                                                                                                           CCLHNCNECQCVPSKVTKKYHEVLQLRPKTGVRGLHKSLTDVALEHHEECDCVCRGSTGG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This invention describes a novel vascular endothelial growth factor-X
                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                           1 AFVFGRKSRVVDLNLLTEEVRLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGGNCA
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                                                                                                                                                                                                                 Length 345;
                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                             ; Score 666; DB 21;
; Pred. No. 5.5e-62;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Dijkmans JJH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     You JR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 72; Fig 12; 127pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB10651 standard; Protein; 345
                                                                                                                                                                                                             100.0%;
100.0%;
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99US-0124967.
99US-0164131.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                 Query Match 100.
Best Local Similarity 100.
Matches 120; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sprengel JJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (JANC ) JANSSEN PHARM NV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human VEGF-X protein #3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2000-442669/38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200037641-A2
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18-MAR-1999;
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Search completed: January 15, 2002, 22:14:47 Job time: 1209 sec

Appl

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Sequence 18, Appl
Sequence 1, Appli
Patent No. 5498600
Sequence 1, Appli
                                                                    Sequence 1, Appli
Patent No. 5428135
Sequence 2, Appli
                                                                                                                        Sequence 2, Al Sequence 2, Al Sequence 27, Bequence 37, Bequence 37, Bequence 27, Bequence 1, Al Sequence 3, Al Al Sequence 3, Al Al
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                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15;
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                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Andrew F. WILKS
APPLICANT: Steven A. STACKER
APPLICANT: Steven A. STACKER
APPLICANT: Kari ALITALO
APPLICANT: Kari ALITALO
ALITALE OF INVENTION: GROWTH FACTOR
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSE: Evenson, McKeown, Edwards & Lenahan P.L.L.C.
STREET: 1200 G Street, NW, Sulte 700
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
APPLICATION DATA:
APPLICATION NUMBER: US/08/915,795
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17.9%; Score 119.5; DB 4; 33.3%; Pred. No. 1.6e-05; iive 15; Mismatches 42;
                                                  5498600-3

US-08-257-494D-1

5428135-2

US-08-989-251-25

US-08-989-251-25

US-09-340-250-2

US-09-989-251-27

US-08-989-251-27

US-08-989-251-27

US-08-340-250-27

US-09-340-250-27

US-09-340-250-27

US-09-340-250-27

US-09-340-250-27
                          PCT-US91-02766-18
PCT-US93-02612-1
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FR: 1064/42983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      United States of America
                                                                                                                                                                                                                                                                                                                                                      Sequence 9, Application US/08915795
Patent No. 6235713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-8800
TELEFAX: (202) 628-8844
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: EVANS, JOSeph D.
REGISTRATION UNMBER: 26,2
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1: 321 amino acids amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mouse Lung
                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Marc G. ACHEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ouery Match 17.9
Best Local Similarity 33.3
Matches 36; Conservative
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CRIGINAL SOURCE:

TISSUE TYPE: Mouse Lu

US-08-915-795-9
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STATE: DC
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TELEX: N/
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Sequence 25, Appl
Sequence 4, Appli
Sequence 6, Appli
Sequence 7, Appli
Sequence 7, Appli
Sequence 29, Appli
Sequence 6, Appli
Sequence 7, Appli
Sequence 24, Appli
Sequence 24, Appli
Sequence 24, Appli
Sequence 54, Appli
Sequence 54, Appli
Sequence 54, Appli
Sequence 54, Appli
                                                                                            ; Search time 24.08 Seconds
(without alignments)
112.143 Million cell updates/sec
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Patent No. 5194596
Patent No. 5175255
Sequence 11, Appl
Sequence 11, Appl
Sequence 11, Appl
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Sequence 15,
Sequence 15,
                                                                                                                                                                                 1 AFVFGRKSRVVDLNLLTEEV......DVALEHHEECDCVCRGSTGG 120
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Sequence 3, 1
Sequence 5, 1
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/cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/pcvuS_COMB.pep:*
/cgn2_6/ptodata/2/iaa/pcvuS_COMB.pep:*
                           Compugen Ltd
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US-08-795-430-57
US-08-609-443B-15
US-08-569-063C-15
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US-08-999-811-6
US-08-778-275-4
US-08-989-251-29
US-09-042-105-6
US-09-340-250-29
US-08-795-430-54
US-08-795-430-54
                                                                                                                                                                                                                                                                               Total number of hits satisfying chosen parameters:
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US-08-915-795-5
US-08-867-352-25
          GenCore version 4.5
Copyright (c) 1993 - 2000 Comp
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US-08-094-079-3
                                                                                                                                                                                                                                                     212252 seqs, 22503292 residues
                                                                                                                                                  US-09-457-066-2_COPY_226_345
666
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                                                                                               22:14:53
                                                                                                                                                                                                                                                                                                                                                   Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                    protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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                                                                                               January 15, 2002,
                                                                                                                                                                                                                                                                                                            length: 0
length: 2000000000
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Match
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Score

NO. Result

107.5 105.5 105.5 105.5 105.5 105.5 105.1

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Minimum DB Maximum DB

Title: Perfect score:

Sequence:

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on:

Scoring table:

Searched:

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GENERAL INFORMATION:
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13 INLLTEEVRLYSCTPRNFSVSIREEL-KRIDTIFWPGCLLVKRCGGNCACCLHNCNECQC
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                                                                                                                                                                                                                                                                                                                                                                                    E: Evenson, McKeown, Edwards & Lenahan P.L.L.C. 1200 G Street, NW, Suite 700
                                                                                              72 V---PSKVTKKYHEVLQLRPKTGVRGLHKSLTDVALEHHEECDCVCRG 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            72 V---PSKVTKKYHEVLQLRPKTGVRGLHKSLTDVALEHHEECDCVCRG 116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
APPLICATION NUMBER: US/08/915,795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17.9%; Score 119.5; DB 4;
33.3%; Pred. No. 1.8e-05;
tive 15; Mismatches 42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            United States of America
                                                                                                                                                                                                                                                                                                                               GROWTH FACTOR
                                                                                                                                                                                                 Sequence 8, Application US/08915795 Patent No. 6235713
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US-08-915-795-3
; Sequence 3, Application US/08915795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: EVANS, Joseph D.
REGIGTRATION NUMBER: 26,269
REFRENCE/DOCKET NUMBER: 1064
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-8800
TELEFAX: (202) 628-8804
                                                                                                                                                                                                                                                    APPLICANT: MAIC G. ACHEN
APPLICANT: Andrew F. WILKS
APPLICANT: Steven A. STACKER
APPLICANT: Kari ALITALO
TITLE OF INVENTION: GROWTH FACT
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 358 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TISSUE TYPE: Mouse Lung
US-08-915-795-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 33.33
Matches 36; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (202) 628-884
TELEX: N/A
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                        Washington
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                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORIGINAL SOURCE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20005
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                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: DC
                                                                                                                                                              RESULT 2
US-08-915-795-8
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 4; Length 325;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: GROWTH FACTOR
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: APORTON, MCKEOWN, Edwards & Lenahan P.L.L.C.
STREET: 1200 G Street, NW, Suite 700
                                                                                                                                                         E: Evenson, McKeown, Edwards & Lenahan P.L.L.C.
1200 G Street, NW, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        44; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     71 CVPSKVTKKYHEVLQLRPKTGVRGLHKSLTDVALEHHEECDCV 113
                                                                                                                                                                                                                                                                                                                                                                          PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. 4.4e-05
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17.3%; Score 115.5; 33.0%; Pred. No. 4.4
                                                                                                                                                                                                                                              United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/915,795
                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC_DOS/MS-DOS
                                                                                         GROWTH FACTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 5, Application US/08915795 Patent No. 6235713
APPLICANT: Marc G. ACHEN
APPLICANT: Andrew F. WILKS
APPLICANT: Steven A. STACKER
APPLICANT: Kari ALITALO
TITLE OF INVENTION: GROWTH FACT
WUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: EVENSON, MCKEOWN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: EVANS, JOSEPH D.
REGISTRATION NUMBER: 26,269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/POCKET NUMBER: 10
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-8800
TELEFAX: (202) 628-884
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APPLICANN: MATC G. ACHEN
APPLICANN: Andrew F. WILKS
APPLICANT: Steven A. STACKER
APPLICANT: Kari ALITALO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human Breast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEX: N/A
INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 325 amino acids
                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
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                                                                                                                                                                                                   Washington
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TISSUE TYPE:
US-08-915-795-3
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                                                                                                                                                                                                                                                               20002
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STATE:
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Gaps

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us-09-457-066-2\_copy\_226\_345.rai

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59 CACCLHNCNECQCVPSKVTKKYHEVLQLRP----KTGV---RGLHKSLTDVALEHHEECD 111
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                                                                                                        5 GRKSRVVDLNLIT--EEVRLYSCTPRN--FSVSIREELKRTDTIF--WPGCLLVKRCGGN 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5 GRKSRVVDLNLLT--EEVRLYSCTPRN--FSVSIREELKRTDTIF--WPGCLLVKRCGGN 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
TITLE OF INVENTION: Preparation of heterodimeric PDGF-AB using a TITLE OF INVENTION: bicistronic vector system in mammalian cells NUMBER OF SEQUENCES: 16
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 16.2%; Score 108; DB 6; Length 220; Best Local Similarity 34.7%; Pred. No. 0.00018; Matches 42; Conservative 12; Mismatches 35; Indels 32;
                     Length 190;
                     16.2%; Score 108; DB 3; Length 190
34.7%; Pred. No. 0.00016;
.ive 12; Mismatches 35; Indels
                                                                                                                                                                                                                                                                                                                                                                                               5175255-4
;Patent No. 5175255
;Patent No. 5175255
; APPLICANT: Thomason, Arlen R.;Nicholson, Margery
; TITLE OF INVENTION: METHODS FOR PURIFICATION OF PLATELET-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPA)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/387,845
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Patent No. 5665567
GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
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                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 9
CURRENT APPLICATION DATA:
  amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13 LNLLTEEVRLYSCTPRNFSVSIREEL-KRTDT1FWPGCLLVKRCGGNCACCLHNCNEC-Q 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: Multicistronic expression units and their use NUMBER OF SEQUENCES: 25
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 4; Length 354;
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPA)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/867,352
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/915,795
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17.3%; Score 115.5; DB 4
Best Local Similarity 33.0%; Pred. No. 4.8e-05;
Matches 34; Conservative 14; Mismatches 44
                                                                                                                                                                                                       CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: EVANS, Joseph D.
RGISTRATION NUMBER: 26,269
REFERENCE/DOCKET NUMBER: 1064/42983
TELECOMMUNICATION INPORMATION:
TELEPHONE: (202) 628-8800
TELEFAX: (202) 628-8844
United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 25, Application US/08867352
Patent No. 6060273
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APPLICATION NUMBER: 08/387,847
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INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 190 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 354 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORIGINAL SOURCE:
TISSUE TYPE: Human Lung
US-08-915-795-5
                                                                                                                                                                                                                                                                                                                                                                            TELEX: N/A
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     single
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                       20002
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  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT
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Gaps

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APPLICANT: Rosen, Craig A.
APPLICANT: Cao, Liang
TITLE OF INVENTION: Polynucelotides Encoding Vascular Endothelial Growth
TITLE OF INVENTION: Pactor 2
FILE REFERENCE: PF112D1
                                                                 79 GRRS----LGSLTIAEPAMIAECKTRTEVFEIS-RRLIDRINANFLVWPPCVEVQRCSG- 132
                                                                                                                                    59 CACCLHNCNECQCVPSKVTKKYHEVLQLRP----KTGV---RGLHKSLTDVALEHHEECD 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           59 CACCLHNCNECQCVPSKVTKKYHEVLQLRP----KTGV---RGLHKSLTDVALEHHEECD 111
                                      GRKSRVVDLNLLT - - EEVRLYSCTPRN - - FSVSIREELKRTDTIF - - WPGCLLVKRCGGN 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5 GRKSRVVDLNLLT--EEVRLYSCTPRN--FSVSIREELKRTDTIF--WPGCLLVKRCGGN 58
                                                                                                                                                                                                                                                                                                                                                                                       Preparation of heterodimeric PDGF-AB using a bicistronic vector system in mammalian cells 16
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 35; Indels
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 Conservative 12; Mismatches
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Patent No. 5938820
PERERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                    Sequence 4, Application US/08778275
Patent No. 5935819
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               241 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 16.2%
Best Local Similarity 34.7%
Matches 42; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Rel. CURRENT APPLICATION DATA: APPLICATION . UWBER: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              , MOLECULE TYPE: protein US-08-778-275-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY:
 42;
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                                                                                                                              32; Gaps
                                                                                                                                                                  5 GRKSRVVDLNLLT--EEVRLYSCTPRN--FSVSIREELKRIDTIF--WPGCLLVKRCGGN 58
                                                                                         Query Match 16.2%; Score 108; DB 1; Length 241; Best Local Similarity 34.7%; Pred. No. 0.0002; Matches 42; Conservative 12; Mismatches 35; Indels
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APPLICANT: ROSEN, CRAIG A.
APPLICANT: CAO, LIANG
TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR 2
NUMBER OF SEQUENCES: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/999,811
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KESSLER, GOLDSTEIN & FOX
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APPLICATION NUMBER: US 08/207,550
FILING DATE: 8-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/465,968
FILING DATE: 06-JUN-1995
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 6, Application US/08999811; Patent No. 5932540; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, G
STREET: 1100 NEW YORK AVENUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 36,351
REFERENCE/DOCKET NUMBER: 146
TELECOMMUNICATION INFORMATION:
TELEPHONE: (2021371-256)
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34.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (202)371-2600
TELEFAX: (202)371-2540
INFORMATION FOR SEQ ID NO: 6:
SEGUENCE CHARACTERISTICS:
LENGTH: 241 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SS: single
not relevant
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                 ; MOLECULE TYPE: protein US-08-387-845-4
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 linear
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Best Local Similarity
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TOPOLOGY:
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COUNTRY:
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APPLICANT: ROSEN, CRAIG A.
APPLICANT: CAO, LIANG
TITLE OF INSURVION: VASCULAR ENDOTHELIAL GROWTH FACTOR 2
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
    35; Indels
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/042,105
FILING DATE: HERRWITH
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  Conservative 12; Mismatches
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APPLICATION NUMBER: US 08/207,550
FILING DATE: 8-MAR-1994
CLASSIFICATION:
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APPLICATION NUMBER: US 08/465,968
FILING DATE: 06-JUN-1995
                                                                                                                                                                                                                                                                                                                                      US-09-042-105-6 Sequence 6, Application US/09042105; Petent No. 6040157; Patent No. 6040157; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 1100 NEW YORK AVENUE CITY: WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REGISTRATION NUMBER: 36,688 REFERENCE/DOCKET NUMBER: 14:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION: (202)371-2600
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APPLICATION NUMBER: TO B:
FILING DATE: 24-DEC-1997
CLASSIFICATION:
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NAME: ERIC K. STEFFE
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not relevant
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STATE: DC
    42;
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                                                                                                                                                                                                                                                                                                                     32;
                                                                                                                                                                                                                                                                        16.2%; Score 108; DB 2; Length 241; 34.7%; Pred. No. 0.0002; ive 12; Mismatches 35; Indels
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Patent No. 6017731
GENERAL INFORMATION:
APPLICANT: Tekamp-Olson, Patricia
TITLE OF INVENTION: METHOD FOR EXPRESSION OF HETEROLOGOUS
TITLE OF INVENTION: PROTEINS IN YEAST
NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
CURRENT APPLICATION NUMBER: US/08/824,996B
CURRENT FILING DATE: 1997-03-27
EARLIER APPLICATION WHER:: 08/207,550
EARLIER FILING DATE: 1994-03-08
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NAME: Spruill, W. Murray
REGISTRATION NUMBER: 32,943
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 919 420 2202
TELEFAX: 919 881 3175
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Best Local Similarity 34.7%
Matches 42; Conservative
                                                                                NUMBER OF SEQ ID NOS: 9
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 8
LENGTH: 241
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                                                                                                                                                                  TYPE: PRT
ORGANISM: Homo sapiens
US-08-824-996-8
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Best Local Similarity
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CITY: Raleigh
STATE: NC
COUNTRY: US
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US-08-989-251-29
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APPLICATION NUMBER:
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Best Local Similarity
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                                                                                                                                                                   FILING DATE:
               27622
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                     59 CACCLHNCNECQCVPSKVTKKYHEVLQLRP----KTGV---RGLHKSLTDVALEHHEECD 111
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GRKSRVVDLNLLT--EEVRLYSCTPRN--FSVSIREELKRTDTIF--WPGCLLVKRCGGN 58
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                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: Multicistronic expression units and their use
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TITLE OF INVENTION: METHOD FOR EXPRESSION OF HETEROLOGGUS
TITLE OF INVENTION: PROTEINS IN YEAST
NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
ADDRESSEE: Bell Seltzer IP Group of Alston & Bird, LLP
STREET: 3605 Glenwood Ave. Suite 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.25 (EPA) CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/867,352
                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS
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CLASSIFICATION
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/387,847
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                                                                                                                                                                                                                                                                             Sequence 4, Application US/08867352
Patent No. 6060273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 4: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 25
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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amino acid
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MOLECULE TYPE: protein
US-08-867-352-4
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Best Local Similarity
Matches 42; Conserv
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PAPLICANT: Joukov, Vaddimir
TITLE OF INVENTION: Vascular Endothelial Growth Factor C (VEGF-C)
TITLE OF INVENTION: Protein and Gene, Mutants Thereof, and Uses Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5 GRKSRVVDLNLLT - - EEVRLYSCTPRN - - FSVSIREELKRTDTIF - - WPGCLLVKRCGGN 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 241;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16.2%; Score 108; DB 3; Length 24:34.7%; Pred. No. 0.0002;
ive 12; Mismatches 35; Indels
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South Wacker Drive
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                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
                                                                                                                                          US/09/340,250
                                           IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 54, Application US/08795430; Patent No. 6130071; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, STREET: 6300 Sears Tower, 233
                                                                                                                                                                                     CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/989,251
                                                                                                                                                                                                                                                                                                     NAME: SPINII, W. MILTAY
REGISTRATION NUMBER: 32,943
REFERENCE/DOCKET NUMBER: 5784
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919 420 2202
TELEPHONE: 919 881 3175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TOPOLOGY: linear; MOLECULE TYPE: protein US-09-340-250-29
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/F196/00427
FILING DAYE: 01-AUG-1996
PRIOR APPLICATION NUMBER: 08/671,573
FILING DATE: 18-JUN-1996
PRIOR APPLICATION NUMBER: 08/601,132
FILING DATE: 18-1996
PRIOR APPLICATION NUMBER: 08/58,895
FILING DATE: 12-JAN-1996
PRIOR APPLICATION NUMBER: 08/58,895
FILING DATE: 12-JAN-1996
PRIOR APPLICATION NUMBER: 08/510,133
FILING DATE: 01-AUG-1995
PRIOR APPLICATION NUMBER: 08/340,011
FILING DATE: 14-NOV-1994
ATONEX APPLICATION NUMBER: 38,153
REGISTRATION NUMBER: 38,153
REGISTRATION NUMBER: 38,153
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REGISTRATION NUMBER: 38,163
REGISTRATION NUMBER: 38,163
RELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-0300
TELERAX: 25-3856
INFORMATION FOR SEQ ID NO: 54:
SEQUENCE CHRRACTERISTICS:
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TYPE: amino acid
STRANDEDNESS: not releva
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MOLECULE TYPE: protein
US-08-795-430-54
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11; 5 GRKSRVVDLNLIT -- EEVRLYSCTPRN -- FSVSIREELKRIDTIF -- WPGCLLVKRCGGN 58 32; Query Match 16.2%; Score 108; DB 4; Length 241; Best Local Similarity 34.7%; Pred. No. 0.0002; Matches 42; Conservative 12; Mismatches 35; Indels Op

59 CACCLHNCNECQCVPSKVTKKYHEVLQLRP----KTGV---RGLHKSLTDVALEHHEECD 111 

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180 C 180

Search completed: January 15, 2002, 22:15:41 Job time: 48 sec

AX164746 Sequence 3 from Pa AX164744 Sequence 1 from Pa AR335584 Homoo sapiens plate AX044487 Sequence 1 from Pa AR336376 Homo sapiens plate

1587 1828 1828 1882 2253

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Ratio: 5.550
Percent Similarity: 100.000
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LOCUS AX027935
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gb_pr:AF335584
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AX0228066 Sequence 60 from Pater
AX028006 Sequence 37 from Pater
AX028089 Sequence 60 from Pater
AX027973 Sequence 41 from Pater
AX028002 Sequence 70 from Pater
AX028070 Sequence 70 from Pater
AX028099 Sequence 70 from Pater
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AF335583 Mus musculus platelet
AB052170 Rattus norvegicus rSC
AB033832 Homo sapiens hSCDGF-E
AX044538 Sequence 52 from Pater
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-Q=Cgn2_1/USPTO_spool/USO457066/runat_15.000 -GAPEXT-4.000
-MINMATCH=0.100 -LOOPCL=0.000 -LOOPEXT=0.000 -FGAPOP=4.500
-GAPEXT=0.050 -XGAPOP=10.000 -XGAPEXT=0.500 -PGAPOP=6.000
-FGAPEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500 -DELOP=6.000
-DELEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500 -PELOP=6.000
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-ALIGN=15 -MODE-LOCAL -OUTFWT=pfs -NORM=ext -HEAPSIZE=500
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-NCPU=6 -ICPU=3 -LONGLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30
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AX028086 Sequence 57 II
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AX027868 Sequence 56 II
AX028064 Sequence 56 II
AX028085 Sequence 56 II
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      out_format : pfs
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AX027989 S
                                                                                 About: Results were produced by the GenCore software, version 4.5, Copyright (c) 1993-2000 Compugen Ltd.
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gb_pat: AX028066
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gb_pat: AX027992
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gb_pr:AX028032
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gb_pat:AX118785
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EUKaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1035)

1 (bases 1 to 1035)

Gordon, R.D., Dijkmans, J.J., Sprengel, J.J., Yon, J.R., Xu, J.,
Gosiewska, A. and Dhanaraj, S.N.
Vascular endothelial growth factor-x
Patent: WO 0037641-A 3 29-JUN-2000;
GORDON ROBERT DOUGLAS (BE); DIJKMANS JOSIENA JOHANNA HUBER (BE);
JANSSEN PHARMACEUTICA NV (BE); SPRENGEL JORG JURGEN (BE); YON
JEFFREY ROLLAND (BE); XU JEAN (US); GOSIEWSKA ANNA (US); DHANARAJ
16-SEP-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                34 leArgGluGluLeuLysArgThrAspThrIlePheTrpProGlyCysLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              rGluGluValArgLeuTyrSerCysThrProArgAsnPheSerValSerI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
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                Sequence 3 from Patent W00037641.
AX027935
AX027935.1 GI:10188752
                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
1. .1035
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US-09-457-066-2_COPY_226_345 x AX027935
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24 - NOV - 2000

PAT

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/protein_id="CAC17170.1"

\[ \frac{1}{2} \text{xref} = \frac{1}{2} \text{3374} \]
\[ \frac{1}{2} \text{xref} = \frac{1}{2} \text{3374} \]
\[ \frac{1}{2} \text{xref} = \frac{1}{2} \text{3374} \]
\[ \frac{1}{2} \text{xref} = \frac{1}{2} \text{xrepresented by CONGYODP} \]
\[ \frac{1}{2} \text{xref} = \frac{1}{2} \text{xref} \text{xrepresented by CONGYODP} \]
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IVMPOFFERAYSPSVLUPPSALDLDLINNAITAFSTLEDLIRYLEBREMOLDLEDDYRP
TWQLLGRAFYFGRASVFORLSSYVDINLITTERYRYSTSTEDLIRELKRTDTIFWGCLL
VKRCGGNCACCLHNCNECQCVPSKVYKKYHEVLQLRPKTGVRGHKSLTDVALEHHEE
                                                                                                                                                                                                                                                                                                     Homo sapiens

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1760)

Gilbert, T., Hart, C.E., Sheppard, P.O. and Gilbertson, D.G.

Growth factor homolog zvegf4

Patent: WO 0066736-A 32 09-NOV-2000;

ZymoGenetics, Inc. (US)

Localicy (US)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 AlaPheValPheGlyArgLySScrArgValValAspLeuAsnLeuLeuTh
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                                                                                                                  AX044518 1760 bp DNA Sequence 32 from Patent WO0066736.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
/db_xref="taxon:9606"
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US-09-457-066-2_COPY_226_345 x AX044518
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Percent Similarity: 100.000
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                                                          seq_name: gb_pat:AX044518
  1026 CACAGGAGGA 1035
                                                                                                               seq_documentation_block:
LOCUS AX044518
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TITLE
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1035)
Gordon, R.D., Dijkmans, J.J., Sprengel, J.J., Yon, J.R., Xu, J.,
Gosiewska, A. and Dhanaraj, S.N.
Vascular endothelial growth factor-x
Patent: WO 0037641-A 29-JUN-2000;
GORDON ROBERT DOUGLAS (BE); DIJKMANS JOSIENA JOHANNA HUBER (BE);
JANSSEN PHARMACEUTICA NV (BE); SPRENGEL JORG JURCEN (BE); YON
STIDEVI NAIDU (US)
LOCATION/QUalifiers
                                                                                                                                                                                                 16-SEP-2000
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Percent Identity: 100.000
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/organism="Homo sapiens"
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a 213 c 251 g 27
                                                                                                                                                                          AXU28032 1035 bp DNA
Sequence 3 from Patent WO0037641.
AX028032
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US-09-457-066-2_COPY_226_345 x AX028032
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Ratio: 5.550
Percent Similarity: 100.000
                                                       1026 CACAGGAGGA 1035
                                                                                                                                                                 seq_name: gb_pr:AX028032
117 rThrGlyGly 120
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FEATURES

ORIGIN

1078

84

50

34

120

Length: Gaps:

u

ACCESSION KEYWORDS SOURCE

VERSION

REFERENCE AUTHORS

FEATURES

CDS

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ICKYDFVEVEDEPSDGTILGRWCGSGTVPGKQISKGNQIRIRFVSDEYFPSEPGFCIHY
WYMPOFFARAYSPSVLAPSALPLDLIANAITAFSTLEDLIRYLDERFWQLDLDEDLYRP
TWQLLGKAFYPGRKSRVDLANLITEFRIKYSCTPRNSSVSIREELKRTDTIFWPGCLL
VKRCGGNCACCLHNCNECQCVPSKVTKXYHEVLQLRPKTGVRGHKKSLTDVALBHEBE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata: Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata: Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1804)

61bertson, D.G., Duff, M.E., West, J.W., Kelly, J.D., Sheppard, P.O., Hofstrand, P.D., Gao, Z., Shoemaker, K., Bukowski, T.R., Moore, M., Feldhaus, A.L., Hummes, J.M., Palmer, T.E. and Hart, C.E. Platelet-derived Growth Factor C (PDGF-C), a Novel Growth Factor J. Biol. Chem. 276 (29), 27406-27414 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 (bases 1 to 1804)
Gao, Z., Hart, C., Piddington, C., Sheppard, P., Shoemaker, K.,
Gilbertson, D., West, J. and O'Hara, P.J.
Direct Submission
Submitted (26-APR-2000) Biomolecular Informatics, ZymoGenetics,
Inc., 1201 Eastlake Avenue East, Seattle, WA 98102, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mkNA PRI 17-JUL-2001 HOMEO Sapiens platelet-derived growth factor C (PDGFC) mRNA, component and control of the 
                                                                  1029 TGAATGTCAATGTCCCAAGCAAAGTTACTAAAAAATACCACGAGGTCC 1078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Percent Identity: 100.000
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/gene="PDGFC"
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Ratio: 5.550
Percent Similarity: 100.000
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LOCUS AF260738
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WYMPOFTARAYSBYLDPSALPLDLIANAITAFSTLEDLIRYLEBERKWOLDLEDIXRP
TWOLLGKRAFYPGRKSRVVDLMLITERYRLYSCTPRNSSYSIRBELKRTDTIFWGCLL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /translation="MSLFGLLLTFSALAGQRQGTQAESNLSSKF0FSSNKEQNGVQDP
QHERIITVSTNGSIHSPRFPHTYPRNTVLVWRLVAVEENVWIQLTFDERFGLEDPEDD
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Gilbertson, D.G.
Gilbertson, D.G.
Patent: WO 0128866-A 1 26-APR-2001; ZymoGenetics, Inc. (US)
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/note="unnamed protein product"
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/db_xref="GI:14035735"
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US-09-457-066-2_COPY_226_345 x AX118785
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/gene="hSCDGF"
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Hamada,T., Ui-Tei,K. and Miyata,Y.

Burect Submission

Submitted (125-02T-1999) to the DDBJ/EMBL/GenBank databases.

Tsuyoshi Hamada, Nippon Medical School, Department of Pharmacology;

1-1-5, Sendagi, Bunkyo-ku, Tokyo 113-8602, Japan

(E-mail:t-hamadaens.ac.jp, Tel:81-3-3822-2131(ex.5277),
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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A novel gene derived from developing spinal cords, SCDGF,
unique member of the PDGF/VEGF family(1)
FEBS Lett. 475 (2), 97-102 (2000)
20317014
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                                                                                                        888 AGAGGAGGTAAGATTATACAGCTGCACACCTCGTAACTTCTCAGTGTCCA
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Homo sapiens embryo brain cDNA to mRNA.
Homo sapiens
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/organism="Homo sapiens'
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/dev_stage="embryo"
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327. 1364
alignment_block:
US-09-457-066-2_COPY_226_345 x AF260738
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327. .1364
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LOCUS AB033831
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CLEARS LATION = "MSIEGLILIFSALAGOROGYQAESNLSSKFOFSSNKEONOOPD OHERITYVSTNGSIHSPRFPHTYPRNTVLVWRLVANEENVWIQLTFDERFGLEDPEDD OHERITYVSTNGSIHSPRFPHTYPRNTVLVWRLVANEENVMIQLTFDERFGLEDPEDD ICKYDFVENEESDGTILGRWCSGTVVGKQISKGNOFRIFRYSDEYFPSEPGFCIHY NIVWPOFFFAVSPSSVLPPSALDFITAFSTLEDLIRYLEPRRWQLDLEDLYR TWQLLGKAFVFGRSRVVDLNLLFEEVRLSCTPRNFSVSIREELKRPDTIFWGCLL VKRCGGNCACCLHNCNECQCVPSKVTKKYHEVLORFRTGVRFKTGVRGLHKSLTDVALEHBE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukarýotá; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Li (bases 1 to 2152)
Li X., Ponten, A., Aase, K., Karlsson, L., Abramsson, A., Uutela, M.,
Backstrom, G., Hellstrom, M., Bostrom, H., Li, H., Soriano, P.,
     cord-derived growth factor'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1002 GCTTTTGTTTTTGGAAGAAATCCAGAGTGGATGGATCTGAACCTTCTAAC 1051
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1052 AGAGGAGGTAAGATTATACAGCTGCACACCTCGTAACTTCTCAGTGTCCA 1101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AspValAlaLeuGluHisHisGluGluCysAspCysValCysArgGlySe 117
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                                                                                                                                                                                                                                                     3 others
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Gaps: 0
Percent Identity: 100.000
                                                                                                                                                                                                                                                     477 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       from: 1 to: 1817
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US-09-457-066-2_COPY_226_345 x AB033831
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                                                                                                                                                                                                                            CDCVCRGSTGG"
                                                                                                                                                                                                                                                     412 c
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Ratio: 5.550
Percent Similarity: 100.000
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1214 CACAGGAGGA 1223

rThrGlyGly 120

117

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/translation="MSI-GGLLLVTSALAGQRRGTQAESNLSSKRQFSSNKEQNGVQDP
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                                                                                                                                                                                                                                                                                                                                              189. 1226
/function="ligand and agonist for platelet-derived growth
factor receptor alpha (PDGFRalpha)
                                                                                                                                                                                                                                                                                                                                                                                                              /note="PDGF-C; member of the PDGF/VEGF growth factor family; contains N-terminal CUB domain and the C-terminal PDGF/VEGF-like domain"
Betsholtz,C., Heldin,C.-H., Alitalo,K., Ostman,A. and Eriksson,U. PDGF-C is a novel protease-activated ligand for the PDGF alpha
                                   receptor
Nat. Cell Biol. (2000) In press
2 (bases 1 to 2152)
2 Eriksson, U., Aase, K., Li, X. and Ponten, A.
Birksson, U., Aase, R., Li, X. and Forten, A.
Direct Submission
Submitted (14-MAR-2000) Ludwig Institute for Cancer Research,
Nobels vag 3 P.O. Box 240, Stockholm S-171 77, Sweden
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /codon_start=1
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/db_xref="G1:8886884"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     964 TAAGGGAAGAACTAAAGAGAACCGATACCATTTTCTGGCCAGGTTGTCTC 1013
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TGAATGTCAATGTGTCCCAAGCAAAGTTACTAAAAAATACCACGAGGTCC 1113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    864 GCTTTTGTTTTGGAAGAAATCCAGAGTGGTGGATCTGAACCTTCTAAC 913
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Gaps: 0
Percent Identity: 100.000
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/tissue_type="lung"
/dev_stage="fetal"
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US-09-457-066-2_COPY_226_345 x AF244813
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Percent Similarity: 100.000
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                                                                                          REFERENCE
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases; 1 to 2849)

Baker, K.P., Chen, J., Ferrara, N., Fong, S., Goddard, A., Gurney, A.L., Hillan, K.J., Kuo, S.S., Tumas, D. and Wood, W.I.

Compositions and methods for the treatment of immune related
                                                     15-DEC-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1060 TAAGGGAAGAACTAAAGAGAACCGATACCATTTTCTGGCCAGGTTGTCTC 1109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          84 euGlnLeuArgProLysThrGlyValArgGlyLeuHisLysSerLeuThr 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  51 LeuValLysArgCysGlyGlyAsnCysAlaCysCysLeuHisAsnCysAs 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        67 nGluCysGlnCysValProSerLysValThrLysLysTyrHisGluValL 84
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                                                                                                                                                                                                                                                                                                   Patent: WO 0070050-A 9 23-NOV-2000;
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                                      AXU47650 2849 bp DNA
Sequence 9 from Patent WO0070050.
AX047650
                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="taxon:9606"
2715
                                                                                                                                                                                                                                                                                                                                                                                                                              /note="unknown base"
                                                                                                                                                                                                                                                                                                                   Genentech, Inc. (US)
Location/Qualifiers
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US-09-457-066-2_COPY_226_345 x AX047650
                                                                                                                                                                                                                                                                                                                                                                                                                                                619 g
                                                                                                        AX047650.1 GI:11876693
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Ratio: 5.550
Percent Similarity: 100.000
seq_name: gb_pat:AX047650
                                                                                                                                                             Homo sapiens
                                  seq_documentation_block:
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                                                                                                                        KEYWORDS
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                                                                                                          VERSION
                                                                                                                                           SOURCE
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117 rThrGlyGly 120

ACCESSION VERSION KEYWORDS

SOURCE

JOURNAL MEDLINE REFERENCE AUTHORS JOURNAL FEATURES

TITLE

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Direct Submission
Submitted (03-JAN-1999) Medical Research, Mackay Memorial Hospital,
45 Min Sheng Road, Tamshui, Taipei 25115, Taiwan
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 2692)
Tsai, Y.-J., Lee, R.K.-K., Chen, Y.-H., Lin, S.-P. and Cheng, W.T.-K.
CDNA cloning of fallotein from mouse ovary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished 2 (bases 1 to 2692)
Tsai,Y.-J., Lee,R.K.-K., Chen,Y.-H., Lin,S.-P. and Cheng,W.T.-K.
                                                                                                                                                                                                                             1317 CFGGTTAAACGCTGTGGGGAACTGTGCCTGTTGTCTCCACAATTGCAA 1366
                                                                                 euGlnLeuArgProLysThrGlyValArgGlyLeuHisLysSerLeuThr 100
                                                              nGluCysGlnCysValProSerLysValThrLysLysTyrHisGluValL
                                                                                                                                                                                                                                                                                                                                                                                                                                              AF117608 2692 bp mRNA ROD
Mus musculus fallotein mRNA, complete cds.
AF117608
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /evidence=not_experimental
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/dev_stage="adult"
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LOCUS AF117608
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SOURCE
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QHERIITVSTNGSIHSPRFPHTYPRNTVLVWRLVAVEENVWIQLTFDERFGLEDPEDD
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TWQLLGGAETVFGRKSRVVDLNLLTEEVRLYSCTPRNFGSYSIREELKRTDTIFWPGCLI
VKRGGGNCACCLHNCNECQCVPSKVTKKYYHEVLQLRFRYTGVRGHKSLTDVALHEE
                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria. Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 3007)

Tsai,Y., Lee,R.K., Lin,S. and Chen,Y.
Identification of a novel platelet-derived growth factor-like gene, fallotein, in the human reproductive tract
Biochim. Biophys. Acta 1492 (1), 196-202 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /evidence-not_experimental
/product="secretory growth factor-like protein fallotein"
/protein_id="AAF00049.1"
/db_xref="G1:602593"
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Trai, Y.J. Lee, R.K.K. and Lin, S.P.
Direct Submission
Submitted (14-SEP-1998) Dept. Medical Research, Mackay Memorial
Hospital, 45 Min Sheng Road, Tamshui, Taipei County 25115, Taiwan
Location/Qualifiers
                                                                                                     AF091434 3007 bp mRNA PRI 22-JUN-2000
Homo sapiens secretory growth factor-like protein failotein mRNA,
complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1167 GCTTTTGTTTTTGGAAGAAATCCAGAGTGGTGGATCTGAACCTTCTAAC 1216
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           34 leArgGluGluLeuLysArgThrAspThrIlePheTrpProGlyCysLeu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /tissue_type="uterus"
492. .1529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       alignment_block:
US-09-457-066-2_COPY_226_345 x AF091434
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613 c
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Percent Similarity: 100.000
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                                                                                                   seq_documentation_block:
LOCUS AF091434
                 1310 CACAGGAGGA 1319
                                                                                                                                                                                                                                                                        Homo sapiens
                                                            seq_name: gb_pr:AF091434
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AUTHORS
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ORIGIN

02-JAN-2000

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ICKYDFVEVEEPSDGSVLGRWCGSGTVPGKQTSKGNHIRIRFVSDEYFPSEPGFCIHY
SIIMPQVTETTSPSVLPPSSLSLDLLNNAVTAFSTLEELIRYLEPDRWQVDLDSLYKP
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Percent Identity: 90.833
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US-09-457-066-2_COPY_226_345 x AF117608
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ZymoGenetics, Inc. (US)
Location/Qualifiers
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98.333
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 3512)

Gao.Z., Hart,C., Piddington,C., Sheppard,P., Shoemaker,K., Gilbertson,D., West,J. and O'Hara,P.J.

Platelet-derived growth factor C (PDGF-C), a novel growth factor that binds to PDGF alpha receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished
2 (bases 1 to 3512)
2 (bases 1 to 3512)
2 (bases 2 to 3512)
3 (albertson, D., West, J. and O'Hara, P.J.
Direct Submission
Submitted (10-MAY-2000) Biomolecular Informatics, ZymoGenetics, Inc., 1201 Eastlake Avenue East, Seattle, WA 98102, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             02-JUN-2001
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growth factor C (Pdgfc) mRNA,
                                                                                                                                                                                                                                                                                                                                                /product="platelet-derived growth factor C"
/protein_id="AAK58566.1"
                                                                                                                                                                                                                                                    1023 CTGGTCAAGCGCTGTGGAGGAATTGTGCCCTGTTGTCTCCCATAATTGCAA 1072
                                                    34
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                                1 AlaPheValPheGlyArgLysSerArgValValAspLeuAsnLeuLeuTh 17
                                                                                                             923 GGAAGAGGTAAAACTCTACAGCTGCACACCCCGGAACTTCTCAGTGTCCCA
                                                                                             17 rGluGluValArgLeuTyrSerCysThrProArgAsnPheSerValSerI
                                                                                                                                                                                                                       LeuvalLysArgCysGlyGlyAsnCysAlaCysCysLeuHisAsnCysAs
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Mus musculus platelet-derived
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AF266467
AF266467.1 GI:14279331
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to: AF117608
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LOCUS AF266467
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seg 1/1
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SOURCE
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 Align
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VKRCGGNCACCLHNCNECQCVPRKVTKKYHEVLQLRPKTGVKGLHKSLTDVALEHHEE
CDCVCRGNAGG"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
1 (bases 1 to 3571)
Gilbert,T., Hart,C.E., Sheppard,P.O. and Gilbertson,D.G.
Crowth Ractor homolog zvegf4
Patent: WO 0066736-A 34 09-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1897 TGAATGTCAGTGTCCCACGTAAAAGTTACAAAAAAGTACCATGAGGTCC 1946
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Gaps: 0
Percent Identity: 90.833
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US-09-457-066-2_COPY_226_345 x AF266467
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alignment_scores:
Quality:
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ORIGIN
AUTHORS
                                  JOURNAL
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                                                                     FEATURES
                                                                                                                                           CDS
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SIIMPQVTETTSPSVLPPSSLSLDLLNNAVTAFSTLEELIRYLEPDRWQVDLDSLYKP
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VKRCGGNCACCLHNCNECQCVPRKVTKKYHEVLQLRPKTGVKGLHKSLTDVALEHHEE
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Sukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
1 (bases 1 to 3571)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1874 CTGGTCAAGCGCTGTGGAGGAAATTGTGCCTGTTGTCTCCATAATTGCAA 1923
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Gaps: 0
Percent Identity: 90.833
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                                               /note="unnamed protein product"
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                                                                                    /protein_id="CAC17171.1"
/db_xref="GI:11343376"
organism="Mus musculus"
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Sequence 3 from Patent WO0128586.
AX118787
            /db_xref="taxon:10090"
1049. .2086
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                                                                     /codon_start=1
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US-09-457-066-2_COPY_226_345
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ACCESSION
                                                                                                                                                                                                                                                BASE COUNT
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ICKYDFVEVEDEPSDGSYLGRWCGSGTVPGKOTSKGNHIRIRRYSDEYFPSEPGFCIHY
SIMPQVTETTSPSVLPPSSLSLDLLINNAVTAFSTLEELIRYLEPDRWQVDLDSLYKP
TWOLLGKAFLYGKKSVVNNLLLKEWKLYSCTPRNFSVSIREEKRUDTIFFMGCLL
VKRCGGNCACCLHNCNECQCVPRKYTKKYHEVLQLRPKTGVKGHKSLTDVALHEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seq_documentation_block:
LOCUS AB033830 1116 bp mRNA
DEFINITION Rattus norvegicus rScdgf mRNA for spinal cord-derived growth
factor, complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1874 CTGGTCAAGCGCTGTGGAGGAAATTGTGCCTGTTGTCTCCCATAATTGCAA 1923
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Percent Identity: 90.833
                                                                                                                               /db_xref="taxon:10090"
11049. 2086
/note="unnamed protein product"
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length:
Gilbertson, D.G.
Method of treating fibrosis
Patent: WO 0128586-A 3 26-APR-2001;
ZymoGenetics, Inc. (US)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                              882
                                                                                                             /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               alignment_block:
US-09-457-066-2_COPY_226_345 x AX118787
                                                                                                                                                                                                                                                                                                                                                                              875 g
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98.333
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AF286725 1038 bp mRNA ROD 23-AUG-2000 Mus musculus platelet-derived growth factor C (Pdgfc) mRNA,
                                                                                                                                              101 AspValAlaLeuGluHisHisGluGluCysAspCysValCysArgGlySe 117
   euGlnLeuArgProLysThrGlyValArgGlyLeuHisLysSerLeuThr
                                                                           AF286725.1 GI:9652343
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5.241
96.667
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1026 CACAGAAGGG 1035
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LOCUS AF286725
                                                                                                                                                                                                                                                                                                                                                        complete cds.
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TITLE
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KEYWORDS
SOURCE
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                                                       84
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="spinal cord-derived growth factor"
protein_id="BAB19969.1"
/db_xref="G1:11994800"
/translation="MLLLGLLLTSALAGQRTGTRAESNLSSKLQLSSDKEQNGVQDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LCKYDFVEVDEPSDGSVLGRWCGSGTVPGKQTSKGNHIRIRFVSDEYFPSEPGFCIHY
SIIMPQVPTSTTSPSYLDPSALSLDLLIMNAYPRASTVEELIRFEDEPRMOIDLOSLYKP
TWPLLGKARIYGKKSRANNINLIKEEVKLYSCTPRWFSVSIREELKRUDTIFWPGCLL
VKRCGGNCACCLHNCNBCQCVPRKVTKKYHEVLQLRPKIGVKGLHKSLTDVALEHHEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RHERVVTISGNGSIHSPKFPHTYPRNTVLVWRLVAVDENVRIQLTFDERFGLEDPEDD
                                                                                                                                         Hamada,T., Ui-Tei,K., Imaki,J. and Miyata,Y.
Molecular Cloning of SCDGF-B, a Novel Growth Factor Homologous to
SCDGF/PDGF-C/fallotein
                                                                        Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                              Hamada,T., Ui-Tei,K. and Miyata,Y.
Direct Submission.
Submitted (25-0CT-1999) Tsuyoshi Hamada, Nippon Medical School, Department of Pharmacology; 1-1-5, Sendagi, Bunkyo-ku, Tokyo 113-8602, Japan (E-mall:t-hamada@nms.ac.jp, Tel:81-3-3822-2131(ex.5277), Fax:81-3-5814-1684)
Location/Qualifiers
AB033830.1 GI:11994799
spinal cord-derived growth factor; SCDGF.
Rattus norvegicus (strain:Wistar) Adult Kidney cDNA to mRNA.
Rattus norvegicus
                                                                                                                                                                                               Biochem. Biophys. Res. Commun. 280 (3), 733-737 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     34 leArgGluGluLeuLysArgThrAspThrIlePheTrpProGlyCysLeu 50
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length: 120
Gaps: 0
Percent Identity: 89.167
                                                                                                                                                                                                                                                                                                                                                                                       /organism="Rattus norvegicus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               262
                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="taxon:10116"
/tissue_type="Kidney"
                                                                    Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-457-066-2_COPY_226_345 x AB033830
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             286 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                         /dev_stage="Adult"
1. .1038
                                                                                                                                                                                                                                                                                                                                                                                                         /strain="Wistar"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="rScdgf"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="rScdgf"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /codon_start=1
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5.267
96.667
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ORIGIN
                                                    ORGANISM
                                                                                                                       REFERENCE
AUTHORS
TITLE
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JOURNAL
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 VERSION
KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CDS
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                                     SOURCE
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Translation="MLLLGLLLTSALAGQRTGTRAESNLSSKLQLSSDKEQNGVQDP RHERVYTISGNGSIHSPKFPHTYPRNWVLVWRLVAVDENVRTGLTFDERFGLEDPEDD ICKYDFVEVEREPSDGSYLGRWGSETYPGKQTSKGNH RIFRYSDEYFPSEPGFCIHY SILMPQVTETTSPSVLPPSSLSLDLLMNAVTAFSTLEELIRYLEPDRWQVDLDSLYKP TWQLLGCAFLYVRKRVVNLNLLKEBVKLYSCTPRNFSSIRELKRYDTRFRYGCLL VKRCGGNCACCLHNCNECQCVPRKYTKKYHEVLQLRPKTGVKGLHKSLTDVALLEE
                                                                                                                                                                                                                                                                                                                                                   Submitted (12-JUL-2000) Samuel Lunenfeld Research Institute, Mount Sinai Hospital, 600 University Avenue, Toronto, Ontario M5G 1X5,
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 1018)
Ding, H., Wu, X., Kim, I., Tam, P.P., Koh, G.Y. and Nagy, A.
The mouse pdgfc gene: dynamic expression in embryonic tissues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="platelet-derived growth factor C"
/protein_id="AAF91483.1"
/db_xref="GI:9652344".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; ·
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="Pdgfc"
/note="PDGFC; similar to PDGF/VEGF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length: 120
Gaps: 0
Percent Identity: 89.167
                                                                                                                                                                                                                                                                                        Ding, H., Wu, X., Tam, P.P.L. and Nagy, A.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /strain="Swiss-Webster/NIH"
/db_xref="taxon:10090"
                                                                                                                                                           during organogenesis
Mech. Dev. 96 (2), 209-213 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Mus musculus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="Pdgfc"
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                                                                                                                                                                                                                                                          (bases 1 to 1038)
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Align seg 1/1 to: AF286725 from: 1 to: 1038

117 rThrGlyGly 120

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This DNA encodes human ZVEGF3 (a novel vascular endothelial growth factor homologue) fused N-terminally to maltose binding protein (MBP). Polypeptides comprising an epitope-bearing portion human or murine and a CUB domain (generic sequence motifs are shown in AAY96859 and AAY96860). The growth factor comprise a growth factor domain and a CUB domain (generic sequence motifs are shown in AAY96859 and AAY96860). The growth factor domain is characterized by an arrangement of cysteine residues and beta-strands that is characteristic of the cysteine knot" structure of the platelet-derived growth factor (PDGF) family. The CUB domain shows homology to CUB domains in neuropilins, human bone morphogenetic protein-1, porcine seminal plasma protein, bovine acidic seminal fluid protein and Xenopus laevis tolloid-like bovine acidic seminal shows homology predict that ZVEGF3 is protein. Structural analysis and homology predict that ZVEGF3 is proteins. The human zvegf3 gene has been mapped to chromosome 4q28.3 zvegF3 is useful for stimulating the growth of fibroblasts or smooth cuscles cells, for activating cell surface PDGF-alpha receptor and for inhibiting PDGF-alpha receptor mediated cellular processes. ZVEGF3 is useful for regulating (post-development) organ growth, regeneration and maintenance, as well as tissue maintenance and repair processes. ZVEGF3 antagonists are useful for treating cancer, rheumatoid arthritis, and characterial intender intimal hyperplasia, atherosclerasis, conditions and contraction and contracti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        nealing, chronic liver disease and haemangioma formation. ZVEGF3 can also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel zvegf3 polypeptides and nucleotides encoding them useful for stimulating growth of smooth muscle cells and fibroblasts comprising epitope bearing portion of a specific amino acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 28; Page 172-173; 173pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
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Chimeric - Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gilbertson DG,
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21-OCT-1999;
12-NOV-1999;
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2668
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                                                                                                                                                                                                            Command line parameters:
-MODEL=frame+_p2n.model -DEV=x1h
-Q=/CQG02_1V10PPTO_spool_/USO9457066/runat_15012002_132155_14243/app_query.fasta_1.190
-DB=N_QCG02_LV10PPTO_spool_/USO9457066/runat_15012002_132155_14243/app_query.fasta_1.190
-DB=N_QCG02_LV10PPTO_spool_/USO9457066/runat_1501000
-GAPEXT=4.000 -MINMATCH=0.100 -LOOPCL=0.000 -LOOPEXT=0.000
-GAPEXT=4.000 -MINMATCH=0.100 -LOOPCL=0.000 -XGAPEXT=0.500
-GAPOP=4.500 -QGAPEXT=0.050 -XGAPOP=10.000 -YGAPEXT=0.500
-FGAPOP=6.000 -FGAPEXT=7.000 -YGAPEXT=0.500
-DELOP=6.000 -DELEXT=7.000 -YAPRT=1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct
-THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=Ffs
-NORM=ext -HEAPSIZE=500 -MINIGN=0 -MAXLEN=2000000000
-USER=USO9457066_eCGN__1_258 -NCPU=6 -ICPU=3 -LONGLOG
-DEV__TIMEOUT=120 -WARN__TIMEOUT=30 -NO_XLPXY -WAIT -THREADS=1
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                       out_format : pfs
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                       to: N_Geneseq_1101:*
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                                                                                                                                   Results were produced by the GenCore Copyright (c) 1993-2000 Compugen Ltd.
of: US:09-457-066-2_COPY_226_345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query: US-09-457-066-2_COPY_226_345
Query length: 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Database sequences: 930621
Database length: 428662619
Search time (sec): 100.840000
                                                                           Date: Jan 15, 2002 11:08 PM
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Shoemaker

Sheppard PO,

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261
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    .5e-50
.2e-49
.4e-45
                                                                                                                                                                                                                                                                                                                                                              Vascular endothelial growth factor; homologue; zvegf3; CUB domain;
                                                                                                                                                                                                                                                                                                                                                                             Cysteine knot; platelet-derived growth factor; PDGF; neuropilin; chromosome 4928 3; cytostatic; anti-psoriatic; anti-inflammatory; anti-diabetic; ophthalmological; anti-rheumatic; anti-arthritic; vulnerary; maltose binding protein; MBP; ss.
    1042.46
1042.46
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513.00 J
513.00 J
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                                                                                                                                seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA2000.DAT:AAA51540
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/SIDS2/gcgdata/geneseq/geneseqn/NA2000.DAT:AAA97807
/SIDS2/gcgdata/geneseqn/Wh2000.DAT:AAA97828
/SIDS2/gcgdata/geneseqn/NA2000.DAT:AAA51499
/SIDS2/gcgdata/geneseq/geneseqn/NA2000.DAT:AA97806
/SIDS2/gcgdata/geneseq/geneseqn/NA2000.DAT:AAA97806
                                                                                                                                                                                                                                                                                                                   MBP-ZVEGF3 fusion protein coding sequence.
                                                                                                                                                                                          ВР
                                                                                                                                                                      seq_documentation_block:
ID AAA51540 standard; cDNA; 1095
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99US-0142576.
99US-0161653.
99US-0165255.
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99WO-US30503

21-DEC-1999;

29-JUN-2000

WO200037641-A2

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VEGF-X; vascular endothelial growth factor; human; vulnerary; cytostatic; antirheumatic; antiarthritic; antipsoriatic; antidiabetic; treatment; angiogenesis regulator; vascularization regulator; cancer; psoriasis; rheumatoid arthritis; diabetic retinopathy; blood vessel; organ repair; tissue regeneration; tissue repair; wound; dermal ulcer; pressure sore;
to modulate neurite growth and development of the nervous system, treating neurodegenerative diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    715 GCTTTTGTTTTGGAAGAAATCCAGAGTGGTGGATCTGAACCTTCTAAC 764
                                                                                                                                                                                                                                                                                                                                                                   815 TAAGGGAAGAACTAAAGAGAACCGATACCATTTTCTGGCCAGGTTGTCTC 864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           euGlnLeuArgProLysThrGlyValArgGlyLeuHisLysSerLeuThr 100
                                                                                                                                                                                                                                                                              1 AlaPheValPheGlyArgLySSerArgValValAspLeuAsnLeuLeuTh 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA2000.DAT:AAA71985
                                                                                                                                                                                                                                                                                                                                                   17 rGluGluValArgLeuTyrSerCysThrProArgAsnPheSerValSerI
                                                                                                                                                                                                                                                                                                                                                                                                                     34 leArgGluGluLeuLysArgThrAspThrIlePheTrpProGlyCysLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         51 LeuValLysArgCysGlyGlyAsnCysAlaCysCysLeuHisAsnCysAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nGluCysGlnCysValProSerLysValThrLysLysTyrHisGluValL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    101 AspValAlaLeuGluHisHisGluGluCysAspCysValCysArgGlySe
                                                     other
                                                                                                                      Length: 120
Gaps: 0
Percent Identity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human VEGF-X DNA for expression in E. coli systems.
                                                    Sequence 1095 BP; 320 A; 227 C; 267 G; 281 T; 0
                                                                                                                                                                                                                                            Align seg 1/1 to: AAA51540 from: 1 to: 1095
                                                                                                                                                                                       alignment_block:
US-09-457-066-2_COPY_226_345 x AAA51540
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Ratio: 5.550
Percent Similarity: 100.000
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                                                                                                      alignment_scores:
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This invention describes a novel vascular endothelial growth factor-X (VEGFX) protein (Ia) and its encoding polynucleotide (IIa) which has vulnerary, cytostatic, antirheumatic, antiarthritic, antipsoriatic and antidiabetic activity and acts as an angiogenesis and vascularization regulator. An antisense molecule of the invention is useful for treating or preventing cancer, rheumatoid arthritis, psoriasis and diabetic retinopathy by inhibiting angiogenic activity or inappropriate vascularization including formation and proliferation of new blood vessels, growth and development of tissues, tissue regeneration and organ and tissue repair in a subject. The products of the invention are useful for preparing medicaments for treating wounds such as dermal ulcers, preparing medicaments for treating wounds such as dermal ulcers, skin graft growth, tissue repair, proliferation of new blood vessels, tissue regeneration and organ repair by promoting anglogenic activity or tissue regeneration and organ repair by promoting anglogenic activity or
                                                                                                                                                                                                                                                                                                                                                                            preventing diseases associated with inappropriate angiogenesis activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       scularization. This sequence encodes a human VEGF-\boldsymbol{x} protein which can expressed in E. coli systems and which is described in the method of
                                                                                                                                                                                                                                                                                                                                                        New vascular endothelial growth factor protein, useful for treating
                                                                                                                                                                                                                                         Ą
                                                                                                                                                                                                                                         Gosiewska
                                                                                                                                                                                                                                                                                                                                                                                                 such as cancer, rheumatoid arthritis, psoriasis and wounds
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps: 0
Percent Identity: 100.000
                                                                                                                                                                                                                                       Dijkmans JJH,
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US-09-457-066-2_COPY_226_345 x AAA71985
                                                                                                                                                                                                                                       You JR,
                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Fig 21; 127pp; English
                                                                                                                   98GB-0028377
                                                                                                                                     99US-0124967.
                                                                                                                                                                                                                                         Sprengel JJ,
                                                                                                                                                                                              (JANC ) JANSSEN PHARM NV
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Ratio: 5.550
Percent Similarity: 100.000
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                                                                                                                                     18-MAR-1999;
08-NOV-1999;
                                                                                                                                                                                                                                                         Dhanaraj SN,
                                                                                                                   22-DEC-1998
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rThrGlyGly 120
                                                                                  the invention.
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 This invention describes a novel vascular endothelial growth factor-X (VEGP-X) protein (Ia) and its encoding polynucleotide (IIa) which has vulnerary, cytostatic, antirheumatic, antiarthritic, antipsoriatic and antidiabetic activity and acts as an antiogenesis and vascularization regulator. An antisense molecule of the invention is useful for treating or preventing cancer, rheumatoid arthritis, psoriasis and diabetic retinopathy by inhibiting angiogenic activity or inappropriate vascularization including formation and proliferation of new blood vessels, growth and development of tissues, tissue regeneration and organ and tissue repair in a subject. The products of the invention are useful
                                                                                                                                                                                                                                                                                                                                                        VEGF-X; vascular endothelial growth factor; human; vulnerary; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New vascular endothelial growth factor protein, useful for treating or preventing diseases associated with inappropriate angiogenesis activity such as cancer, rheumatoid arthritis, psoriasis and wounds -
                                                                                                                                                                                                                                                                                                                                                                  antirheumatic; antiarthritic; antipsoriatic; antidiabetic; treatment, and openesis regulator; vascularization regulator; cancer; psoriasis; rheumatoid arthritis; diabetic retinopathy; blood vessel; organ repair; tissue regeneration; tissue repair; wound; dermal ulcer; pressure sore; venous sore; diabetic ulcer; burns; skin graft growth; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sprengel JJ, Yon JR, Dijkmans JJH, Gosiewska A;
                                                                                               seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA2000.DAT:AAA71983
                          101 AspValAlaLeuGluHisHisGluGluCysAspCysValCysArgGlySe
890 IGAATGTCAATGTCCCAAGCAAAGTTACTAAAAAATACCACGAGGTCC
                                                                                                                                                                                                                                                                                                                            DNA for expression in mammalian systems.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
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                                                                                                                                                                                                                           seq_documentation_block:
ID AAA71983 standard; DNA; 1134 BP
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99US-0124967.
99US-0164131.
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                                                                                                                                                                                                                                                                                                (first entry)
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                                                                                                                                                           1040 CACAGGAGGA 1049
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                                                                                                                                                                                                                                                                                                                            Human VEGF-X
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-DEC-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gordon RD,
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for preparing medicaments for treating wounds such as dermal ulcers, pressure sores, venous sores, diabetic ulcers and burns and to promote skin graft growth, tissue repair, proliferation of new blood vessels, tissue regeneration and organ repair by promoting angiogenic activity or vascularization. This sequence encodes a human VEGF-X protein which can be expressed in mammalian systems and which is described in the method of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VEGF-X; vascular endothelial growth factor; human; vulnerary; cytostatic; anticheumatic; antiatthritic; antipsoriatic; antidiabetic; treatment; angiogenesis regulator; vascularization regulator; cancer; psoriasis; rheumatoid arthritis; diabetic retinopathy; blood vessel; organ repair; tissue regeneration; tissue repair; wound; dermal ulcer; pressure sore; venous sore; diabetic ulcer; burns; skin graft growth; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human VEGF-X DNA for expression in Baculovirus/insect cell systems.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              734
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17 rGluGluValArgLeuTyrSerCysThrProArgAsnPheSerValSerI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      euGlnLeuArgProLysThrGlyValArgGlyLeuHisLysSerLeuThr
                                                                                                                                                                                                                                 294 T; 0 other;
                                                                                                                                                                                                                                                                                                                                            Length: 120
Gaps: 0
Percent Identity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              from: 1 to: 1134
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G
                                                                                                                                                                                                                                 247 C; 269
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US-09-457-066-2_COPY_226_345 x AAA71983
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                                                                                                                                                                                                                                 Sequence 1134 BP; 324 A;
                                                                                                                                                                                                                                                                                                                                          Quality: 666.00
Ratio: 5.550
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              to: AAA71983
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915 CTGGTTAAACGCTGTGGTGGAACTGTGCCTGTTGTCTCCACAATTGCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (VEGE-X) protein (Ta) and its encoding polynucleotide (IIa) which has vulnerary, cytostatic, antirheumatic, antiarthritic, antipsoriatic and antidabetic activity and acts as an angiogenesis and vascularization regulator. An antisense molecule of the invention is useful for treating or preventing cancer, rheumatoid arthritis, psoriasis and diabetic retinopathy by inhibiting angiogenic activity or inappropriate vascularization including formation and proliferation of new blood vessels, growth and development of tissues, tissue regeneration and organ at issue repair in a subject. The products of the invention are useful for preparing medicaments for treating wounds such as dermal ulcers, pressure sores, venous sores, diabetic ulcers and burns and to promote skin graft growth, tissue repair, proliferation of new blood vessels, tissue regeneration and organ repair by promoting angiogenic activity or vascularization. This sequence encodes a human VEGE-X protein which can be expressed in Baculovirus/insect cell systems and which is described in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New vascular endothelial growth factor protein, useful for treating or preventing diseases associated with inappropriate angiogenesis activity such as cancer, rheumatoid arthritis, psoriasis and wounds -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This invention describes a novel vascular endothelial growth factor-X
                                                                                                                                                                                                                                                                                                                                                                          Gosiewska A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       765 GCTTTTGTTTTGGAAGAAAATCCAGAGTGGTGGATCTGAACCTTCTAAC 814
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17 rGluGluValArgLeuTyrSerCysThrProArgAsnPheSerValSerI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1134 BP; 339 A; 225 C; 254 G; 316 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length: 120
Gaps: 0
Percent Identity: 100.000
                                                                                                                                                                                                                                                                                                                                                                          Sprengel JJ, Yon JR, Dijkmans JJH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Align seg 1/1 to: AAA71984 from: 1 to: 1134
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US-09-457-066-2_COPY_226_345 x AAA71984
Location/Qualifiers
63..1127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Fig 20; 127pp; English
                                                              "VEGF-X"
                                                                                                                                                                                                                                                            99US-0124967.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the method of the invention.
                                                                                                                                                                                             99WO-US30503
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                                        /*tag= a
/product=
                                                                                                                                                                                                                                                                                                                             (JANC ) JANSSEN PHARM NV.
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Percent Similarity: 100.000
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                                                                                                         WO200037641-A2
                                                                                                                                                                                                                                      22-DEC-1998;
18-MAR-1999;
08-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                Dhanaraj SN,
                                                                                                                                                                                             21-DEC-1999;
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                                                                                                                                                   29-JUN-2000
                                                                                                                                                                                                                                                                                                                                                                          Gordon RD,
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Human, VEGF/PDGF-like factor; vascular endothelial growth factor; VEGF; platelet derived growth factor; PDGF; neovascularisation; disease; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence is a novel vascular endothelial growth factor (VBGF)/platelet derived growth factor (PBGF)-like factor. The invention relates to the present 345 amino acid sequence or as sequence in which at least one amino acid is deleted, replaced or added compared to the present sequence. The nucleotide sequence encoding this protein may be integrated into a vector and used to transform a host cell. The VBGF/PBGF-like factor may be used to development of agents for treating diseases associated with
                                                                                                                                                                       1064
84 euGlnLeuArgProLysThrGlyValArgGlyLeuHisLysSerLeuThr 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA2001.DAT:AAF82259
                                                                                                                                               Sequence 1328 BP; 372 A; 288 C; 324 G; 344 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              seq_documentation_block:
ID AAF82259 standard; DNA; 1328
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Ratio: 5.550
Percent Similarity: 100.000
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Jan

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P-PSDB; AAB10635, AAB10636.
VEGF-X; vascular endothelial growth factor; human; vulnerary; cytostatic; antirheumatic; antiarthritic; antipsoriatic; antidiabetic; treatment; anglogenesis regulator; vascularization regulator; cancer; psoriasis; rheumatoid arthritis; diabetic retinopathy; blood vessel; organ repair; tissue regeneration; tissue repair; wound; dermal ulcer; pressure sore;
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                                                                                                                                                                                                                                                                                     euGlnLeuArgProLysThrGlyValArgGlyLeuHisLysSerLeuThr 100
                                                                venous sore; diabetic ulcer; burns; skin graft growth; ds.
                                                    1 AlaPheValPheGlyArgLysSerArgValValAspLeuAsnLeuLeuTh 17
                                                                                                                                                                                                                                                                                                                                                                                                          seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA2000.DAT:AAA71955
                                                                                                                                         AGAGGAGGTAAGATTATACAGCTGCACACCTCGTAACTTCTCAGTGTCCA
                                                                                                                                                                                                                                                                                                                    101 AspValAlaLeuGluHisHisGluGluCysAspCysValCysArgGlySe
                                                                                               rGluGluValArgLeuTyrSerCysThrProArgAsnPheSerValSerI
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to
          US-09-457-066-2_COPY_226_345 x AAF82259
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ID AAA71955 standard; DNA; 1473
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99US-0164131
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                               to: AAF82259
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08-NOV-1999;
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alignment_block
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                               Align seg 1/1
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This invention describes a novel vascular enocurellar grown factor. A (VEGE-X) protein (Ia) and its encoding polynucleotide (IIa) which has vulnerary, cytostatic, antirheumatic, antiarthritic, antipsoriatic and inflabetic activity and acts as an angiogenesis and vascularization regulator. An antisense molecule of the invention is useful for treating or preventing cancer, rheumatoid arthritis, psoriasis and diabetic retinopathy by inhibiting angiogenic activity or inappropriate vascularization including formation and proliferation of new blood vessels, growth and development of tissues, tissue regeneration and organ and tissue repair in a subject. The products of the invention are useful for preparing medicaments for treating wounds such as dermal ulcers, pressure sores, wenous sores, diabetic ulcers and burns and to promote skin graft growth, tissue repair, proliferation of new blood vessels, tissue regeneration and organ repair play promoting angiogenic activity or vascularization. This sequence encodes the human vEGF-X protein isolated from clones 4 and 7 described in the method of the invention.
New vascular endothelial growth factor protein, useful for treating or preventing diseases associated with inappropriate angiogenesis activity such as cancer, rheumatoid arthritis, psoriasis and wounds -
                                                                                                                                                                                                              This invention describes a novel vascular endothelial growth factor-X
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TAAGGGAAGAACTAAAGAGAACCGATACCATTTTCTGGCCAGGTTGTCTC 1081
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      rGluGluValArgLeuTyrSerCysThrProArgAsnPheSerValSerI 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA2000.DAT:AAC81582
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1473 BP; 406 A; 321 C; 361 G; 385 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-457-066-2_COPY_226_345 x AAA71955
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           from: 1
                                                                                                                                          Claim 4; Fig 9; 127pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Quality: 666.00
Ratio: 5.550
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           to: AAA71955
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           rThrGlyGly 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   alignment_scores
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           alignment_block
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Align seg 1/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                101
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CUB domain; PDGF-like activity; mitogenic; osteogenic; osteogenic; neovascularisation; tissue repair; proliferation; differentiation; niver damage; neuroregenerative; Alzheimer's disease; multiple sclerosis; periodontal disease; bone fracture; wound healing; vulnerary; ischaemia; immunomodulation; hepatic; ds.
                                                                                                                                                                                                                                                      fusion; growth factor homologue; VEGF/PDGF family;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Growth factor homologs and the nucleic acids that encode them, useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            e.g. for treating liver damage, ischemia, multiple sclerosis and Alzheimer's disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gilbertson DG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 25; Page 123-125; 143pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sheppard PO,
AAC81582 standard; DNA; 1760 BP
                                                                                                                                                                                        Human zveqf3 DNA, SEQ ID NO:32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        03-MAY-1999; 99US-0304216.
10-NOV-1999; 99US-0164463.
04-FEB-2000; 2000US-0180169.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 03-MAY-2000; 2000WO-US40047
                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (ZYMO ) ZYMOGENETICS INC.
                                                                                                                                                                                                                                                      Human; zvegf3; zvegf4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gilbert T, Hart CE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2000-687541/67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P-PSDB; AAB48657
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200066736-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
                                                                                                                           09-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   09-NOV-2000
                                                             AAC81582
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979

29

51

LeuValLysArgCysGlyGlyAsnCysAlaCysCysLeuHisAsnCysAs

978

34 leArgGluGluLeuLysArgThrAspThrIlePheTrpProGlyCysLeu

67

84

20

829 GCTTTTGTTTTGGAAGAAATCCAGAGTGGTGGATCTGAACCTTCTAAC 878

rGluGluValArgLeuTyrSerCysThrProArgAsnPheSerValSerI

17

to: AAC81582 from: 1 to: 1760

Align seg 1/1

alignment\_block: US-09-457-066-2\_COPY\_226\_345 x AAC81582

Percent Identity: 100.000

Gaps:

Quality: 666.00 Ratio: 5.550 Percent Similarity: 100.000

alignment\_scores

1029 TGAATGTCAATGTCTCCCAAGCAAAGTTACTAAAAAATACCACGAGGTCC 1078

nGluCysGlnCysValProSerLysValThrLysLysTyrHisGluValL

euGlnLeuArgProLysThrGlyValArgGlyLeuHisLysSerLeuThr 100

84

1079 TICAGTIGAGACCAAAGACCGGTGTCAGGGGATIGCACAAATCACTCACC 101 AspValAlaLeuGluHisHisGluGluCysAspCysValCysArgGlySe

117 rThrGlyGly 120

1129

The invention relates to the human growth factor homologue zvegf4

(AAB48653), and nucleic acids encoding it (AAC81555). Zvegf4 is a member

of the PDGF (platelet-derived growth factor)/VEGF (vascular endothelial

growth factor) family. Zvegf4 has a growth factor domain (AAB48654)

c dracterised by a PDGF cystine knot structure, and a CUB domain

c characterised by a PDGF cystine knot structure. Zvegf4 has PDGF-like.

CC AAA88655) which has a beta barrel structure. Zvegf4 has PDGF-like.

activity, having mitogenic activity on fibroblasts, vascular smooth

cc activity, having mitogenic activity on fibroblasts, vascular smooth

cc activity, having mitogenic activity on fibroblasts, vascular smooth

cc yegf4 or fragments thereof, particularly human zvegf4 human zvegf3

ct usions: expression constructs and host cells comprising human

cc yegf4 or fragments thereof, particularly human zvegf4, an antibody

which binds to human zvegf4 or a fragment thereof; a method of activating

c a cell-surface PDGF receptor using a zvegf4-derived polypeptide; an

method of modulating the proliferation of human injuration or

c a cell-surface PDGF receptor using a xepgf4-derived polypeptide; an

method of modulating the proliferation of factoring a genetic

companilty in the zvegf4 gene of a patient. Zvegf4 proteins and derived

cr zvegf4-derived polypeptides; and a method of detecting a genetic

companilty in the zvegf4 gene of a patient. Zvegf4 proteins and derived

cr zvegf4-derived polypeptides; and a method of Alzheiner's disease or

cc abnormality in the zvegf4 gene of a patient. Zvegf4 proteins and creative growth (e.g., in the treatment of serion or proliferation. They are particularly used for

cc alular enurite growth (e.g., in the treatment of Alzheiner's disease or

multiple sclerosis). Due to their osteogenic activity, they may be used to

condulate neurite growth (e.g., in the treatment of serion or serion of the immine svetem cells in the

cused to enhance expansion and mobilisation of haemacles or munimum of schemen immune system. The present sequence represents DNA encoding human

Sequence 1760 BP; 494 A; 373 C; 411 G; 482 T; 0 other;

99WO-US28968

07-DEC-1999;

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Vascular endothelial growth factor; homologue; zvegf3; CUB domain; Cysteine knot; platelet-derived growth factor; PDGF; neuropilin; chromosome 4q28.3; cytostatic; anti-psoriatic; anti-inflammatory; anti-diabetic; ophthalmological; anti-rheumatic; anti-arthritic;
                       seq_name: /SIDS2/qcqdata/qeneseq/qeneseqn/NA2000.DAT:AAA51498
                                                                                                                              Human growth factor homologue, ZVEGF3, cDNA.
                                                                                                                                                                                                                                                   Location/Qualifiers
154..1191
                                                          AAA51498 standard; cDNA; 1760 BP
                                                                                                                                                                                                                                                                          /*tag= a
/product= ZVEGF3
154..195
                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                              /*tag=
CACAGGAGGA 1188
                                               seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                     WO200034474-A2
                                                                                                                                                                                                      vulnerary; ss
                                                                                                                                                                                                                              Homo sapiens
                                                                                                        26-SEP-2000
                                                                                                                                                                                                                                                                                                                                                            15-JUN-2000.
                                                                                                                                                                                                                                                                                                  sig_peptide
1179
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Z

Gao

This

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Human; Zvegf3 antagonist; cell proliferation; stellate cell activation; extracellular matrix production; fibrosis; VEGF-R; POGF-C; platelet-derived growth factor; PDGF; vascular endothelial growth factor; VEGF, mitogenic effect; therapy; keloid; scleroderma; fibrotic disorder; chronic active hepatitis; fulminant viral hepatitis; amyloidosis; diabetic nephropathy; alpha-1-antirypsin deficiency; silicosis; asbestosis; renal arteriosclerosis; post necrotic cirrhosis; diabetic glomerulosclerosis; focal glomerulosclerosis; hyperostosis; bulmonary fibrosis; obteopetrosis; bronchiolitis obliterans-organising pneumonia; transplant vasculopathy; fibroproliferative disorder; ds.
979 CTGGTTAAACGCTGTGGTGGGAACTGTGCCTGTTGTCTCCCACAATTGCAA 1028
                                                               seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA2001.DAT:AAD04649
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product= "Mature human 2vegf3 protein"
                                                                                                                             euGlnLeuArgProLysThrGlyValArgGlyLeuHisLysSerLeuThr
                                                                                                                                                   nGluCysGlnCysValProSerLysValThrLysLysTyrHisGluValL
                                                                                                                                                                                                                 101 AspValAlaLeuGluHisHisGluGluCysAspCysValCysArgGlySe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Human Zvegf3 protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAD04649 standard; DNA; 1760 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12-NOV-1999; 99US-0165255.
01-AUG-2000; 2000US-022223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23-OCT-2000; 2000WO-US29270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-OCT-1999; 99US-0161653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     04-JUL-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /*tag= a
/product=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /*tag= b
196..1188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (ZYMO ) ZYMOGENETICS INC.
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                                                                                                                                                                                                                                                                                                                                        CACAGGAGGA 1188
                                                                                                                                                                                                                                                                                                                                                                                                                                seq_documentation_block:
                                                                                                                                                                                                                                                                                                  117 rThrGlyGly 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human Zvegf3 DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P-PSDB; AAE00997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200128586-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gilbertson DG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26-APR-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mat_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAD04649;
                                                                                   1029
                                                                                                                                                                                                                                                        1129
                                                                                                                                                                                                                                                                                                                                          1179
                                         67
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                                                                                                                                                                       1079
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                      designated ZVECF3 are claimed. The growth factors comprise a growth human or murine ZVECF3 are claimed. The growth factors comprise a growth factor domain and a CUB domain in Generic sequence motifs are shown in AXY96859 and AXY96860). The growth factor domain is characterized by an arrangement of cysteine residues and beta-strands that is characteristic of the "cysteine knot" structure of the platelet derived growth factor (PDGF) family. The CUB domain shows homology to CUB domains in neurophlins, human bone morphogenetic protein. Up porcine seminal plasma protein. Structural analysis and homology predict that ZVEGF3 polypeptides complex with a second polypeptide to form multimeric proteins. The human zvegf3 gene has been mapped to chromosome 4q28.3. ZVEGF3 is useful for stimulating the growth of fibroblasts or smooth muscles dells, for activating cell surface PDGF-alpha receptor and for inhibiting PDGF-alpha receptor mediated cellular processes. ZVEGF3 is useful for regulating (post-development) organ growth, regeneration and maintenance, as well as tissue maintenance and repair processes. ZVEGF3 antagonists are useful for treating cancer, rheumatoid arthritis, disbemia, vascular intimal hyperplasia, attended to a structure growth and for disease, myocardial ischemia, vascular intimal hyperplasia, attended to a second to mediate neurite growth and for development of the nervous system, and for treating neurodegenerative
                                                                                                                                                                                                                                                                                              Novel zvegf3 polypeptides and nucleotides encoding them useful for stimulating growth of smooth muscle cells and fibroblasts comprising an epitope bearing portion of a specific amino acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                             cDNA encodes a human vascular endothelial growth factor homologue,
                                                                                                                                                                       Shoemaker KE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               878
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        rGluGluValArgLeuTyrSerCysThrProArgAsnPheSerValSerI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1760 BP; 494 A; 373 C; 411 G; 482 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Percent Identity: 100.000
                                                                                                                                                                       Sheppard PO,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Align seg 1/1 to: AAA51498 from: 1 to: 1760
                                                                                                                                                                                                                                                                                                                                                                                    Claim 29; Page 146-148; 173pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       alignment_block:
US-09-457-066-2_COPY_226_345 x AAA51498
                                                                                                                                                                  Piddington CS,
                                     99US-0142576.
99US-0161653.
99US-0165255.
                   98US-0207120
                                                                                                                             (ZYMO ) ZYMOGENETICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Quality: 666.00
Ratio: 5.550
Percent Similarity: 100.000
                                                                                                                                                                                        West JW;
                                                                                                                                                                                                                                WPI; 2000-423420/36.
P-PSDB; AAY96858.
                                                                                                                                                                       CE,
                                                                                                                                                                                        Gilbertson DG,
                                                                                                                                                                       Hart
                                                                                   12-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    alignment_scores:
                                       06-JUL-1999;
21-OCT-1999;
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of

Use of zvegf3 antagonist for reducing fibroproliferative disorder kidney, liver and bone, reducing extracellular matrix production, treating fibrosis or reducing stellate cell activation in mammal

929 TAAGGGAAGAACTAAAGAGAACCGATACCATTTTCTGGCCAGGTTGTCTC 978

17

LeuValLysArgCysGlyGlyAsnCysAlaCysCysLeuHisAsnCysAs

21

cDNA encoding platelet-derived growth factor C (PDGF-C).

(first entry)

25-JUL-2000

AAA12523;

 $\mathbf{x} \overset{\mathsf{A}}{\otimes} \mathbf{x} \overset{\mathsf{A}}{\otimes} 0$ 

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proliferation or extracellular matrix production, treating fibrosis and reducing stellate cell activation in a mammal. The method comprises administering a composition in a mammal. The method comprises administering a composition containing a Yvegf3 antagonist in combination with a delivery vehicle. The Zvegf3 is a protein that is structurally related to platelet-derived growth factor (PDGF) and the vascular endothelial growth factors (VEGF). The Zvegf3 protein is also designated as "VEGF-R" and "PDGF-C". The Zvegf3 antagonist is useful to block the mitogenic effects of zvegf3 and thereby to inhibit or prevent and treat keloids, scleroderma, fibrotic disorders of liver such as chronic active hepatitis, fulminant viral hepatitis, post necrotic cirrhosis and alpha-1-antitrypsin defliciency, fibrotic disorders of the kidney such as diabetic glomerulosclerosis, focal glomerulosclerosis, diabetic nephropathy, amyloidosis and renal arteriosclerosis, fibrotic disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             of the lung such as silicosis, asbestosis, idiopathic pulmonary fibrosis, bronchiolitis obliterans-organising pneumonia and pulmonary hypertension, fibrotic disorders of pancreas, fibroproliferative disorders of the vasculature such as transplant vasculopathy and fibroproliferative disorders of the bone such as osteopetrosis and hyperostosis. The present sequence is human 2vegf3 DNA.
                                                                     patent discloses materials and methods for reducing cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1029 TGAATGTCAATGTGCCCAAGCAAAGTTACTAAAAAATACCACGAGGTCC 1078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             829 GCTTTTGTTTTTGGAAGAAAATCCAGAGTGGTGGATCTGAACCTTCTAAC 878
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    50
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17 rGluGluValArgLeuTyrSerCysThrProArgAsnPheSerValSerI 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  34 leArgGluGluLeuLysArgThrAspThrIlePheTrpProGlyCysLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LeuValLysArgCysGlyGlyAsnCysAlaCysCysLeuHisAsnCysAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     nGluCysGlnCysValProSerLysValThrLysLysTyrHisGluValL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           101 AspValAlaLeuGluHisHisGluGluCysAspCysValCysArgGlySe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1760 BP; 494 A; 373 C; 411 G; 482 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length: 120
Gaps: 0
Percent Identity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             from: 1 to: 1760
Example 1; Page 54-56; 70pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 alignment_block:
US-09-457-066-2_COPY_226_345 x AAD04649
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Quality:
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carcinoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PDGF-C polypeptide can be enzymatically processed to generate the active truncated form of PDGF-C and used to regulate the receptor-binding specificity of PDGF-C and also be used to promote fibroblast mitogenesis in a mammal and to induce PDGF alpha receptor activation. PDGF-C antagonists can be used to inhibit tumour growth of a tumour
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel DNA encoding PDGF-C useful to stimulate or enhance proliferation, differentiation, growth and motility of cells expressing the PDGF-C \,
                                                                                                                                 growth factor; heparin; connective tissue; wound healing; VEGF-F; fibroblast mitogenesis; PDGF alpha receptor activation; tumour growth; choriocarcinoma; Wilms tumour; megakaryoblastic leukaemia; lung carcinoma; erythroleukemia; tissue remodelling; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence encodes human platelet-derived growth factor C (PDGF-C) (formally designated VBGF-F). PDGF-C polypeptides have the ability to stimulate and enhance proliferation or differentiation, and/or growth or motility of cells expressing a PDGF-C receptor. PDGF-C polypeptides can be used in pharmaceuticals for promoting cell proliferation, preferably in combination with one other growth factor and heparin. Pharmaceuticals complising PDGF-C polypeptides can also be used for stimulating connective tissue or wound healing. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                expressing PDGF-C in a mammal. Specific types of human tumours, e.g. choriocarcinoma, Wilms tumour, megakaryoblastic leukaemia, lung carci and erythroleukemia, can be identified by testing for expression of PDGF-C PDGF-C antagonists can also be used to inhibit tissue remodelling during invasion of tumour cells into a normal population cells. Antagonists can also be used to treat fibrotic conditions, especially found in the lung, kidney or liver.
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                                                                                                                   Platelet-derived growth factor C; PDGF-C; cell proliferation;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Uutela M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ponten A,
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Betsholz C;
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98US-0108109.
98US-0110749.
98US-0113002.
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Heldin C,
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P-PSDB; AAY84557.
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                                                                                                                                                                                                                           Homo sapiens
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alignment\_scores:

seq\_name: /SIDS2/gcgdata/geneseq/geneseqn/NA2000.DAT:AAA12523

seq\_documentation\_block:
ID AAA12523 standard; cDNA; 2108 BP

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This invention describes a novel vascular endothelial growth factor-X (VEGF-X) protein (Ia) and its encoding polynucleotide (IIa) which has vulnerary, cytostatic, antirheumatic, antiartitic, antipsoriatic and antidiabetic activity and acts as an angiogenesis and vascularization regulator. An antisense molecule of the invention is useful for treating corperventing cancer, rheumatoid arthritis, psoriasis and diabetic retinopathy by inhibiting angiogenic activity or inappropriate vascularization including formation and proliferation of new blood vessels, growth and development of tissues, tissue regeneration and organ and tissue repair in a subject. The products of the invention are useful for preparing medicaments for treating wounds such as dermal ulcers, pressure sores, venous sores, diabetic ulcers and burns and to promote skin graft growth, tissue repair, proliferation of new blood vessels, tissue regeneration and organ repair, proliferation of new blood vessels, the sequence encodes the RACE generated human VEGF-X vertices.
                                                                                                                                                                                                                          New vascular endothelial growth factor protein, useful for treating or preventing diseases associated with inappropriate angiogenesis activity such as cancer, rheumatoid arthritis, psoriasis and wounds -
                                                                                                        Yon JR, Dijkmans JJH, Gosiewska A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                84 euGlnLeuArgProLysThrGlyValArgGlyLeuHisLysSerLeuThr 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               rGluGluValArgLeuTyrSerCysThrProArgAsnPheSerValSerI
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US-09-457-066-2_COPY_226_345 x AAA71951
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      99US-0124967
                        99US-0164131
                                                                                                      Sprengel JJ,
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                                                               (JANC ) JANSSEN PHARM NV
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Ratio: 5.550
Percent Similarity: 100.000
                                                                                                                           Xu J;
                                                                                                                                                                  WPI; 2000-442669/38
                                                                                                                                                                                  P-PSDB; AAB10633
                                                                                                                         Dhanaraj SN,
      18-MAR-1999;
08-NOV-1999;
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                                                                                                      RD,
                                                                                                      Gordon
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      VEGF-X; vascular endothelial growth factor; human; vulnerary; cytostatic; antirheumatic; antiarthritic; antipsoriatic; antidiabetic; treatment; angiogenesis regulator; vascularization regulator; cancer; psoriasis; rheumatolid arthritis; diabetic retinopathy; blood vessel; organ repair; tissue regeneration; tissue repair; wound; dermal ulcer; pressure sore; venous sore; diabetic ulcer; burns; skin graft growth; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   911
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                        Gaps: 0
Percent Identity: 100.000
      Length:
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                                                                            alignment_block:
US-09-457-066-2_COPY_226_345 x AAA12523
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human RACE generated VEGF-X DNA
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                                                                                                                                           Align seg 1/1 to: AAA12523
666.00
5.550
100.000
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    Quality:
Ratio:
                                       Percent Similarity:
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21

962 67 912 84

17

29

120

Gaps:

1041

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67

84

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1092 CTGGTTAAACGCTGTGGTGGGAACTGTGCCTGTTGTCTCCACAATTGCAA 1141
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                                                                                                                                                                                                                                                                                                                                                  942 GCTTTTGTTTTTGGAAGAAATCCAGAGTGGTGGATCTGAACCTTCTAAC
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                                                                                       Percent Identity: 100.000
                                Length:
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                                                                                                                                                    alignment_block:
US-09-457-066-2_COPY_226_345 x AAA71990
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ID AAA71952 standard; DNA; 2776 BP
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                                                          Ratio: 5.550
Percent Similarity: 100.000
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   alignment_scores
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                VEGF-X; vascular endothelial growth factor; human; vulnerary; cytostatic; antirheumatic; antiarthritic; antipsoriatic; antidiabetic; treatment; angiogenesis regulator; vascularization regulator; cancer; psoriasis; rheumatoid arthritis; diabetic retinopathy; blood vessel; organ repair; tissue regeneration; tissue repair; wound; dermal ulcer; pressure sore; venous sore; diabetic ulcer; burns; skin graft growth; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New vascular endothelial growth factor protein, useful for treating or preventing diseases associated with inappropriate angiogenesis activity such as cancer, rheumatoid arthritis, psoriasis and wounds -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gosiewska A;
                                                                                                                    seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA2000.DAT:AAA71990
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267..1304
/*tag= a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product= "VEGF-X"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Yon JR,
                                                                                                                                                                                                                 AAA71990 standard; cDNA; 2668 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98GB-0028377.
99US-0124967.
99US-0164131.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99WO-US30503
                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (JANC ) JANSSEN PHARM NV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sprengel JJ,
                                WPI; 2000-442669/38
                                                                                                                                                                                    seq_documentation_block:
117 rThrGlyGly 120
                                                                                                                                                                                                                                                                                                                                                                                                         Human VEGF-X cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P-PSDB; AAB10644
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WO200037641-A2

21-DEC-1999;

29-JUN-2000

22-DEC-1998; 18-MAR-1999; 08-NOV-1999;

Homo sapiens

19-JAN-2001

AAA71990;

Dhanaraj SN,

Gordon RD,

A COURT COUR

117

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VEGF-X; vascular endothelial growth factor; human; vulnerary; cytostatic;
                                                                                               antirheumatic; antiarthritic; antipsoriatic; antidiabetic; treatment; angiogenesis regulator; vascularization regulator; cancer; psoriasis; rheumatoid arthritis; diabetic retinopathy; blood vessel; organ repair; tissue regeneration; tissue repair; wound; dermal ulcer; pressure sore; venous sore; diabetic ulcer; burns; skin graft growth; ds.
                                                                                                                                                                                                                                                          /product= "VEGF-X homologue"
                                                                                                                                                                                                                                                                                        WO200037641-A2
                                                                                                                                                                                                                                                                                                                    29-JUN-2000
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Sequence 2668 BP; 780 A; 511 C; 567 G; 810 T; 0 other;

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This invention describes a novel vascular endothelial growth factor-X
(VEGF-X) protein (Ia) and its encoding polynucleotide (IIa) which has
vulnerary, oytostatic, antirheumatic, antipsoriatic and
antidiabetic activity and acts as an anglogenesis and vascularization
cegulator. An antisense molecule of the invention is useful for treating
regulator. An inhibiting anglogenic activity or inappropriate
or preventing cancer, rheumatoid arthritis, psoriasis and diabetic
retinopathy by inhibiting anglogenic activity or inappropriate
vascularization including formation and proliferation of new blood
vessels, growth and development of tissues, tissue regeneration and organ
and tissue repair in a subject. The products of the invention are useful
for preparing medicaments for treating wounds such as dermal ulcers,
for preparing medicaments for treating wounds such as dermal ulcers,
for preparation and organ repair, proliferation of new blood vessels,
tissue regeneration and organ repair by promoting anglogenic activity or
vascularization. This sequence encodes the human VEGF-X protein homologue
described in the method of the invention.
                                                                                                                                                                                                                                                                                                                    preventing diseases associated with inappropriate angiogenesis activity such as cancer, rheumatoid arthritis, psoriasis and wounds \mbox{-}
                                                                                                                                                                                                                                                                                                  New vascular endothelial growth factor protein, useful for treating
                                                                                                                                                                        Gosiewska A;
                                                                                                                                                                        Dijkmans JJH,
                                                                                                                                                                        You JR,
                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Fig 7; 127pp; English.
                                                           99US-0124967.
99WO-US30503
                                          98GB-0028377
                                                                                                                                                                      Sprengel JJ,
                                                                                                                            (JANC ) JANSSEN PHARM NV
                                                                                                                                                                                                                                  2000-442669/38.
                                                                                                                                                                                                                                                          P-PSDB; AAB10634
                                                                                                                                                                      Gordon RD, S
Dhanaraj SN,
                                                              18-MAR-1999;
21-DEC-1999;
                                          22-DEC-1998;
                                                                                  38-NOV-1999;
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Sequence 2776 BP; 825 A; 515 C; 587 G; 849 T; 0 other;

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Percent Identity: 100.000
                           Gaps:
            Length:
         Quality: 666.00
Ratio: 5.550
Percent Similarity: 100.000
alignment_scores
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alignment\_block: US-09-457-066-2\_COPY\_226\_345 x AAA71952

Baughn MR;

Guegler KJ,

Corley NC,

Yue H, Hillman JL,

WPI; 2000-350695/30.

Au-Young J;

Tang YT,

P-PSDB; AAB03003

1 AlaPheValPheGlyArgLysSerArgValValAspLeuAsnLeuLeuTh 17

from: 1 to: 2776

to: AAA71952

Align seg 1/1

rGluGluValArgLeuTyrSerCysThrProArgAsnPheSerValSerI 17

985 AGAGGAGGTAAGATTATACAGCTGCACACCTCGTAACTTCTCAGTGTCCA 1034

84 nGluCysGlnCysValProSerLysValThrLysLysTyrHisGluValL 67

euGlnLeuArgProLysThrGlyValArgGlyLeuHisLysSerLeuThr 100 84

cardiovascular disorder; bacterial infection; viral; fungal; parasitic; cancer; allergy; asthma; arteriosclerosis; therapy; diagnosis; consensus; reproductive tissue; reproductive tissue; developmental disorder; cell proliferative disorder; immune disorder; reproductive disorder; Human GFRP-4; growth factor related molecule; diseased breast tissue; bone morphogenetic protein 1; BMP-1; inflammation; immune response; AspValAlaLeuGluHisHisGluGluCysAspCysValCysArgGlySe 117 cDNA encoding human growth factor related molecule GFRP-4. seq\_name: /SIDS2/gcgdata/geneseq/geneseqn/NA2000.DAT:AAA52458 /\*tag= a /product= "Human GFRP-4" Location/Qualifiers 258..1295 BP AAA52458 standard; cDNA; 2779 98US-0181711. 98US-0209547. 99US-0313457. 99WO~US25458 (first entry) (INCY-) INCYTE PHARM INC. 1285 CACAGGAGGA 1294 seq\_documentation\_block: rThrGlyGly 120 WO200024774-A2 28-OCT-1998; 11-DEC-1998; 17-MAY-1999; Homo sapiens 28-OCT-1999; 25-SEP-2000 04-MAY-2000 AAA52458; 117 101 SS. 

This sequence represents cDNA encoding human growth factor related molecule GFRP-4. cDNA encoding GFRP-4 was initially identified in a diseased breast tissue cDNA library, and the present sequence represents a consensus derived from several overlapping and/or extended cDNA clones. GFRP-4 has chemical and structural homology with human bone morphogenetic protein 1 (BMP-1) (27% identity at the BMP-1 C-terminus). GFRP-4 was found by Northern analysis to be expressed in reproductive and cardiovascular tissue, and in cDNA libaries associated with cancer, inflammation and the immune response. GFRP proteins (AAB03000-B03003), nucleotides encoding them (AAA52455-A55458), GFRP gronists and antagonists may be used to treat a wide variety of diseases associated with increased or decreased expression or activity of GFRP proteins. Conditions which may be treated include developmental disorders, cell Human growth factor related molecule protein useful for the diagnosis and treatment of disorders associated with its activity including developmental, cell proliferative, immune, reproductive and cardiovascular disorders and infections -Claim 9; Page 76; 80pp; English.

or

/product= "VEGF-E"

99WO-US05190 98US-0040220 98US-0184216

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New growth factor polypeptide useful for treating cardiovascular endothelial disorders, e.g. cardiac hypertrophy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 34 leArgGluGluLeuLysArgThrAspThrIlePheTrpProGlyCysLeu 50
                                                                                                                                                                                                                                                                                                    Claim 2; Fig 1; 122pp; English.
                                                                                                                                                         (GETH ) GENENTECH INC
                                                                                                                                                                                                                WPI; 1999-580306/49.
                                                                                                                                                                                       Ferrara N, Kuo SS;
                                                                                                                                                                                                                                P-PSDB; AAY33679
                              W09947677-A2
                                                                                    10-MAR-1999;
                                                                                                                               02-NOV-1998;
                                                                                                                17-MAR-1998
                                                          23-SEP-1999
    proliferative disorders (e.g., cancers), immune disorders (e.g., allergies, asthma), reproductive disorders (e.g., menstrual cycle disorders) cardiovascular disorders (e.g., arteriosclerosis) and bacterial, viral, fungal or parasitic infections. Additionally, GFRP proteins and nucleotides can be used in the diagnosis of such disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VEGF-E; human; vascular endothelial cell growth factor; wound repair; treatment; cardiovascular disorder; endothelial disorder; therapy; tissue generation; regeneration; cardiac hypertrophy; cancer; detection; angiogenic disorder; age-related macular degeneration; vascular disease; neovascularization; tumor; gene mapping; ss.
                                                                                                                                                                                                                                                                                                                                             1033 TAAGGGAAGAACTAAAGAGAACCGATACCATTTTCTGGCCAGGTTGTCT 1082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1133 TGAATGTCAATGTCTCCCAAGCAAAGTTACTAAAAAATACCACGAGGTCC 1182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   84 euGlnLeuArgProLysThrGlyValArgGlyLeuHisLysSerLeuThr 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               101 AspValAlaLeuGluHisHisGluGluCysAspCysValCysArgGlySe 117
                                                                                                                                                                                                                                                                                       933 GCTTTTGTTTTTGGAAGAAAATCCAGAGTGGTGGATCTGAACCTTCTAAC 982
                                                                                                                                                                                                                                                                                                                             17 rGluGluValArgLeuTyrSerCysThrProArgAsnPheSerValSerI 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 67 nGluCysGlnCysValProSerLysValThrLysLysTyrHisGluValL 84
                                                                                                                                                                                                                                                                       1 AlaPheValPheGlyArgLysSerArgValValAspLeuAsnLeuLeuTh 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA1999.DAT:AA223691
                                                                                                                                                                                                                                                                                                                                                                                     34 leArgGluGluLeuLysArgThrAspThrIlePheTrpProGlyCysLeu
                                                                                    Sequence 2779 BP; 832 A; 515 C; 585 G; 847 T; 0 other;
                                                                                                                                           Length: 120
Gaps: 0
Percent Identity: 100.000
                                                                                                                                                                                                                                             to: 2779
                                                                                                                                                                                                 alignment_block:
US-09-457-066-2_COPY_226_345 x AAA52458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                             from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seq_documentation_block:
ID AAZ23691 standard; DNA; 2825 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  259..1296
                                                                                                                                           Quality: 666.00
Ratio: 5.550
Percent Similarity: 100.000
                                                                                                                                                                                                                                             Align seg 1/1 to: AAA52458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1283 CACAGGAGGA 1292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     117 rThrGlyGly 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human VEGF-E DNA.
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                                                                                                                               alignment_scores
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  8 X C C C C C C
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This invention describes the isolation of a novel human vascular endothelial cell growth factor-E (VEGF-E) polypeptide which has transported and properties of transported and transported and the administered therapeutically, especially by expressing encoding polynucleotides, to treat cardiovascular or endothelial disorders in mammals, especially humans. It is useful in wound repair and tissue generation and regeneration, and may especially be used to treat cardiac hypertrophy it can be combined with a carrier in pharmaceutical compositions, which can be administered to treat disorders as above. VEGF-E can be used to screen for antagonists and agonists, and the antagonists administered to treat angiogenic disorders in mammals (especially humans) e.g. cancer or reat angiogeneration. It can be used to generate antibodies, useful therapeutically as antagonists, as above. The antibodies are also useful to detect VEGF-E polypeptide, especially to diagnose cardiovascular, endothelial or angiogenic disorders in mammals (e.g. vascular disease, or neovascularization associated with tumor formation of an antibody-VEGF-E polypeptide complex. Polynucleotides encoding VEGF-E can be used to diagnose cardiovascular and endothelial disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            in mammals, by detecting abnormally high or low VEGF-E gene expression in tissue samples. They can also be used to diagnose a disease or susceptibility to a disease related to a mutated form of VEGF-E (e.g. a cardiovascular, endothelial or angiogenic disorder such as a tumor), by detecting a mutation in the VEGF-E-encoding sequence isolated from a sample. They may also be used to produce probes useful to detect related sequences or for gene mapping. This sequence encodes the human VEGF-E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                984 AGAGGAGGTAAGATTATACAGCTGCACACCTCGTAACTTCTCAGTGTCCA 1033
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2825 BP; 849 A; 522 C; 605 G; 848 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Percent Identity: 100.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length:
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US-09-457-066-2_COPY_226_345 x AA223691
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Quality: 666.00
Ratio: 5.550
Percent Similarity: 100.000
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1034 TAAGGAAGAACTAAAGAGAACCGATACCATTTCTGGCCAGGTTGTCT 1083
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- 117 rThrGlyGly 120

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                                                                        seq_name: /cgn2_6/ptodata/2/ina/6B_COMB.seq:US-08-915-795-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        nucleic acid
                                                                                                                                                                                                                                                          Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
                                                                                                                                   GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                               COUNTRY: Ur
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APPLICANT:
                                                                                                                                                                                                                                                                       STATE:
                                                                                                                                                                                                                                                          CITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    731 : Pate
739 : Pate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         691 ! Pater
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                                                                                                                                                                                                                                                                                                                                                                                               868
868
868
 out_format : pfs
                                                About: Results were produced by the GenCore software, version 4.5, Copyright (c) 1993-2000 Compugen Ltd.
OM of: US-09-457-066-2_COPY_226_345 to: Issued_Patents_NA:*
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Query length: 120
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Search time (sec): 38.750000
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                         Date: Jan 15, 2002 11:06 PM
                                                                                                                                                                                                                                                                                                        Database sequences: 351203
                                                                                                                                                                                                                                                        Search information block:
                                                                                   Command line parameters:
                                                                                                                                                                                                                                                                                                                                                                                            Seguence
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APPLICANT: Andrew F. WILKS
APPLICANT: Steven A. STACKER
APPLICANT: Kari ALITAN
TITLE OF INVENTION: GROWTH FACTOR
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Evenson, MCKeown, Edwards & Lenahan P.L.L.C.
STREET: 1200 G Street, NW, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |||::::::::: ||||||| :::
389 CTAAAAGTTATAGATGAAAAAGGAGGACCCAATGCAGGGCCTAGAGA 438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13 LeuAsnLeuLeuThrGluGluValArgLeuTyrSerCysThrProArgAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29 nPheSerValSerIleArgGluGluLeu...LysArgThrAspThrIleP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Percent Identity: 33.333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           to: 1135
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               alignment_block:
US-09-457-066-2_COPY_226_345 x US-08-915-795-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        to: US-08-915-795-7 from: 1
                                                                                                                                                                                                                                                                                                                                                                          United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/915,795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PC-DOS/MS-DOS
seq_documentation_block:
    Sequence 7, Application US/08915795
    Patent No. 6235713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: EYANS, Joseph D.
REGISTRATION NUMBER: 26, 269
REFERENCE/DOCKET NUMBER: 1064,
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-8800
TELEFAX: (202) 628-8844
                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORIGINAL SOURCE:
TISSUE TYPE: Mouse Lung
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 1135 base pairs
                                                                                                       Marc G. ACHEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEX: N/A
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Quality: 119.50
Ratio: 1.927
Percent Similarity: 57.407
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530 TGC....AACGAAGAGGGTGTGATGTGTATGAACACAAGCACCTCCTA 573
                                                                                                                                                                                                                      574 CATCTCCAAACAGCTCTTTGAGATATCAGTG.....CCTCTGACATCAG 617
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45 heTrpProGlyCysLeuLeuValLysArgCysGlyGlyAsnCysAlaCys 61
                                                                                                                                                                          75 sValThrLysLysTyrHisGluValLeuGlnLeuArgProLysThrGlyV 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      & Lenahan P.L.L.C.
                                                                                        62 CysLeuHisAsnCysAsnGluCysGlnCysVal.....ProSerLy 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                seq_name: /cgn2_6/ptodata/2/ina/6B_COMB.seq:US-08-915-795-6
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Percent Identity: 33.333
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/915,795
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                                           489 TCAAGCCCCCTGTGTAAATGTCTTCCGGTGTGGAGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Evenson, McKeown, Edwards
STREET: 1200 G Street, NW, Suite 700
CITY: Washington
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Marc G. ACHEN
APPLICANT: Andrew F. WILKS
APPLICANT: Steven A. STACKER
APPLICANT; Kari ALITALO
TITLE OF INVENTION: GROWTH FACTOR
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                          109 GluCysAspCysValCysArgGly 116
                                                                                                                                                                                                                                                                                                                                                                                   656 GGTTGTAAGTGCTTGCCCACGGGC 679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seq_documentation_block:
; Sequence 6, Application US/08915795
; Patent No. 6235713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: EVANS, JOSEPH 26, 269
RECISTRATION NUMBER: 26, 269
REFERENCE/DOCKET NUMBER: 1064,
TELECPHONICATION INFORMATION:
TELEPHONE: (202) 628-8800
TELEFAX: (202) 628-8844
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEX: N/A
INFORMATION FOR SEQ ID NO: (
SEQUENCE CHARACTERISTICS:
LENGTH: 1325 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORIGINAL SOURCE:
TISSUE TYPE: Mouse Lung
US-08-915-795-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             119.50
1.927
57.407
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Ratio:
Percent Similarity:
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391 CTAAAAGTTATAGATGAAGAAGGAGCAGAGGACCCAATGCAGGGA 440
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576 CATCTCCAAACAGCICTITGAGATATCAGIG......CCTCTGACAICAG 619
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                                                                                                                             13 LeuAsnLeuLeuThrGluGluValArgLeuTyrSerCysThrProArgAs 29
                                                                                                                                                                                                                               29 nPheSerValSerIleArgGluGluLeu...LysArgThrAspThrIleP 45
                                                                                                                                                                                                                                                                                                                             45 heTrpProGlyCysLeuLeuValLysArgCysGlyGlyAsnCysAlaCys 61
                                                                                                                                                                                                                                                                                                                                                                                                                               62 CysLeuHisAsnCysAsnGluCysGlnCysVal.....ProSerLy 75
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STREET: 1200 G Street, NW, Suite 700
                                                                                                                                                                                                                                                                                                                                                       seq_name: /cgn2_6/ptodata/2/ina/6B_COMB.seq:US-08-915-795-4
                                                                            to: US-08-915-795-6 from: 1 to: 1325
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alignment_block:
US-09-457-066-2_COPY_226_345 x US-08-915-795-6
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APPLICANT: Steven A. STACKER
APPLICANT: KATI ALITALO
TITLE OF INVENTION: GROWTH FACTOR
WUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
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Patent No. 6235713
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               658 GGTTGTAAGTGCTTGCCCACGGGC 681
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MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS.
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TELECOMMUNICATION INFORMATION
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(202) 628-8844
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NAME: EVANS, Joseph D.
REGISTRATION NUMBER: 26,3
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LENGTH: 2029 base pairs
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94 lyLeuHisLysSerLeuThrAspValAlaLeuGluHisHisGluGluCys 110
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                                                                                                                                                                                                                                                                               Percent Identity: 33.010
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
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US-09-457-066-2_COPY_226_345 x US-08-915-795-4
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Fatent No. 6235713
GENERAL INFORMATION:
APPLICANT: Marc G. ACHEN
APPLICANT: Steven A. STACKER
APPLICANT: Karl ALITALO
TITLE OF INVENTION: GROWTH FACTOR
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            United States of America
                                                                                 HYPOTHETICAL: NO
ORIGINAL SOURCE:
TISSUE TYPE: Human Lung
US-08-915-795-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                   115.50
1.925
58.252
                        single
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    nucleic acid
                                                                  CDNA
                                              linear
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TYPE: nucleic
STRANDEDNESS:
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Ratio:
Percent Similarity:
                                                               MOLECULE TYPE:
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                                         TOPOLOGY:
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2209 .....ccrgaattagrgccrgrraaagrrgccaarcaracaggrrgr 2250
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Patent No. 6017731
GENERAL INFORMATION:
APPLICANT: Tekamp-Olson, Patricia
TITLE OF INVENTION: METHOD FOR EXPRESSION OF HETEROLOGOUS
TITLE OF INVENTION: PROTEINS IN YEAST
NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
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Percent Identity: 33.010
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US-09-457-066-2_COPY_226_345 x US-08-915-795-1
APPLICATION NUMBER: US/08/915,795
FILING DATE:
CLASSIFICATION: 536
ATTORNEY AGENT INFORMATION:
NAME: EVANS, JOSEPH D.
REGISTRATION NUMBER: 26,269
REGISTRATION NUMBER: 1064/42983
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-8800
                                                                                                                                              1064/42983
                                                                                                                                                                                                                                     TELEX: N/A
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2846 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE TYPE: Human Breast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             115.50
1.925
58.252
                                                                                                                                                                                                                                                                                                                                                                                    linear
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MOLECULE TYPE:
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66 GACCACTTGGCTTGTAAGTGT 46
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ORIGINAL SOURCE:
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Ratio:
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MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                     COUNTRY: US
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                                                                                                                                                                                                                                                                                              CITY:
STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DLESCRIPTION: /desc = "Complementing strand to the DESCRIPTION: preceding SEQ ID NO:, listed to show the terminal overhangs DESCRIPTION: produced upon assembly."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           to reverse of: US-08-989-251-4 from: 1 to: 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          324 ATCGCTGAACCAGCTATGATCGCTGAATGTAAGACTAGAACTAAGTTTTC 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          274 GAAATCTCCAGAAGATTCGALCGACAGAACTAACGCTAACTTCTGGTTT 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              147 ......CAATTGAGACCAGTTCAAGTTAGAAAGATCGAAA 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  92 al......ArgGlyLeuHisLysSerLeuThrAspValAlaLeuGlu 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31 rValSerIleArgGluGluLeuLysArgThrAspThrIlePhe..... T 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .....LysThrGlyV 92
ADDRESSEE: Bell Seltzer IP Group of Alston & Bird, LLP STREET: 3605 Glenwood Ave. Suite 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16 LeuThrGluGluValArgLeuTyrSerCysThrProArg...AsnPheSe 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          rpProGlyCysLeuLeuValLysArgCysGlyGlyAsnCysAlaCysCys 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        63 LeuHisAsnCysAsnGluCysGlnCysValProSerLysValThrLysLy 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps: 8
Percent Identity: 33.645
                                                                                                                                                                            SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                alignment_block:
US-09-457-066-2_cOPY_226_345 x US-08-989-251-4/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     79 sTyrHisGluValLeuGlnLeuArgPro.....
                                                                                                                                                                                                                                     US/08/989, 25
                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: SPRUILL, W. WARTAY
REGISTRATION NUMBER: 32,943
REFERENCE/DOCKET NUMBER: 5784
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919 420 2202
TELEPHONE: 919 881 3175
                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             106 HisHisGluGluCysAspCys 112
                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 352 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                               CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     112.00
1.867
56.075
                                                                                                                                                        COMPUTER: IBM PC
OPERATING SYSTEM:
SOFTWARE: PatentI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
                                                                                                                                                                                                                                                                          CLASSIFICATION:
                                  Raleigh
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MOLECULE TYPE:
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                                                                             COUNTRY:
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                                                      STATE:
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DESCRIPTION: /desc = "Complementing straing to the terminal overhangs DESCRIPTION: preceding SEQ ID NO:, listed to show the terminal overhangs DESCRIPTION: produced upon assembly."
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                                                                 Sequence 4, Application US/09340250
Patent No. 6083723
GENERAL INFORMATION:
APPLICANT: Tekamp-Olson, Patricia
TITLE OF INVENTION: METHOD FOR EXPRESSION OF HETEROLOGOUS
TITLE OF INVENTION: PROTEINS IN YEAST
NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     274 GAAATCTCCAGAAGATTCGATCGACAGAACTAACGCTAACTTCTTGGTTT 225
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                                                                                                                                                                                                                                                                                                    ADDRESSEE: Bell Seltzer IP Group of Alston & Bird, LLP STREET: 3605 Glenwood Ave. Suite 310
seg_name: /cgn2_6/ptodata/2/ina/6A_COMB.seg:US-09-340-250-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/340,250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Percent Identity: 33.645
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US-09-457-066-2_COPY_226_345 x US-09-340-250-4/rev
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Spruill, W. Murray
REGISTRATION NUMBER: 32,943
REFERENCE/DOCKET NUMBER: 571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
TELEPHONE: 919 420 2202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Spruill, W. Murray
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 352 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 919 881 3175 INFORMATION FOR SEO ID NO:
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1.867
56.075
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SEQ ID NO:3:
LENGTH: 691
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Multicistronic expression units and their use
                                                                92 al......ArgGlyLeuHisLysSerLeuThrAspValAlaLeuGlu 105
224 GGCCACCATGTGTTGAAGTTCAAAGATGTTCTGGT......TGTTGT 184
                                                                                                                      79 sTyrHisGluValLeuGlnLeuArgPro.....LysThrGlyV 92
                                         63 LeuHisAsnCysAsnGluCysGlnCysValProSerLysValThrLysLy 79
                                                                                                                                                                                                                          5 GlyArgLysSerArgValValAspLeuAsnLeuLeuThr.....GluGl 19
                                                                                                                                                                                                                                                                                                                                                                 seq_name: /cgn2_6/ptodata/2/ina/6A_COMB.seq:US-08-867-352-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: mat_peptide
LOCATION: 283..609
OTHER INFORMATION: /product= "mature PDGF-B chain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length: 121
Gaps: 11
Percent Identity: 34.711
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US-09-457-066-2_COPY_226_345 x US-08-867-352-24
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OTHER INFORMATION: /product= "PDGF-B
OTHER INFORMATION: precursor sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/867,352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: Multicistronic NUMBER OF SEQUENCES: 25
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 24, Application US/08867352
Patent No. 6060273
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/387,847
                                                                                                                                                                                                                                                                                    106 HisHisGluGluCysAspCys 112
                                                                                                                                                                                                                                                                                                                         66 GACCACTTGGCTTGTAAGTGT 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IMMEDIATE SOURCE:
CLONE: pSBC-1/-2-PDGF-B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 625 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
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54.545
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MOLECULE TYPE: c
ORIGINAL SOURCE:
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Ratio:
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LOCATION: 40.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
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.crgggtrcccrgaccarrgcrgagcc 311
                                                                                                                                                                                                                                                                                       312 GGCCATGATCGCCGAGTGCAAGACGCGCACCGAGGTGTTCGAGATCTCC. 360
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1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 11
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                                                                                                                                                                      19 uValArgLeuTyrSerCysThrProArgAsn.....PheSerValSerI 34
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;Patent No. 517525;
APAPLIC.AS17525;
; TITLE OF INVENTION: METHODS FOR PURIFICATION OF PLATELET:
; TITLE OF INVENTION: METHODS FOR PURIFICATION OF PLATELET.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19 uValArgLeuTyrSerCysThrProArgAsn.....PheSerValSerI
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Percent Identity: 34.711
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US-09-457-066-2_COPY_226_345 x 5175255-3
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/06/25,344
FILING DATE: 23-MAR-1987
                                               274 GGAAGAAGGAGC.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Align seg 1/1 to: 5175255-3
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Ratio: 1.636
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108 uGluCysAspCys 112

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seq_documentation_block:
;Patent No. 5194596
; APPLICANT TISCHER, EDMUND G.;ABRAHAM, JUDITH A.;FIDDES, JOHN
; ATTLE OF INVENTION: PRODUCTION OF VASCULAR ENDOTHELIAL CELL
; TITLE OF INVENTION: PRODUCTION OF VASCULAR ENDOTHELIAL CELL
                                                                                                                                                                                                                93 ... ArgGlyLeuHisLysSerLeuThrAspValAlaLeuGluHisHisGl 108
                                                                                                                                                                                                                                           322 ..cegecercaragaceceaeceaeceaerrecregreresecece 369
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                                                                                                                                                              376 ......CAGCTGCGACCTGTCCAGGTGAGAAGATCGAGATTGTGCGG 417
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235 GGAAGAAGGAGC......CTGGGTTCCCTGACCATTGCTGAGCC 272
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273 GGCCATGATCGCCGAGTGCAAGACGCGCACCGAGGTGTTCGAGATCTCC. 321
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                                                                                                        82 luValLeuGlnLeuArgPro.....LysThrGlyVal....
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Gaps: 11
Percent Identity: 34.711
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                                                    342 CAACCGCAACGTGCAGTGCCGCCCCACCCAGGTG
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US-09-457-066-2_COPY_226_345 x 5194596-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/07/450,883
FILING DATE: 14-DEC-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 387,545
FILING DATE: 27-JUL-1989
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54.545
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Percent Similarity:
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Patent No. 5219739

APPLICANT: TISCHER, EDMUND G.; ABRAHAM, JUDITH A.; FIDDES, JOHN C.; MITCHELL, RICHARD L.

TITLE OF THE SEQUENCES ENCODING BVEGF120 AND ; HVEGF 121 AND METHODS FOR THE PRODUCTION OF BOVINE AND HUMAN ; HVEGF 121 AND METHODS CELL GROWTH FACTORS, BVEGF120 AND HVEGF121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              243 GGAAGAAGGAGC......CTGGGTTCCCTGACCATTGCTGAGCC 280
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                                                  seq_name: /cgn2_6/ptodata/2/ina/backfiles1.seq:5219739-14
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                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/07/559,041
FILING DATE: 27-JUL-1990
REIOR APPLICATION DATA:
APPLICATION NUMBER: 450,883
FILING DATE: 14-DEC-1989
APPLICATION NUMBER: 387,545
FILING DATE: 27-JUL-1989
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US-09-457-066-2_COPY_226_345 x 5219739-14
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54.545
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528 GGCATGCAAGTGT 540
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                                                                                                     seq_documentation_block:
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; LENGTH: 739
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FEBS Lett.
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                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
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VOLUME:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AUTHORS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product= "PDGF-B
precursor sequence"
/note= "human PDGF-B gene from pGEM2-PDGF-B,
flanked by 5'-ECORI und 3'-HindIII
restriction cleavage sites"
                                                              Preparation of heterodimeric PDGF-AB using a bicistronic vector system in mammalian cells
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   34 leArgGluGluLeuLysArgThrAspThrIlePhe.....TrpProGly 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5 GlyArgLysSerArgValValAspLeuAsnLeuLeuThr.....GluGl 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19 uValArgLeuTyrSerCysThrProArgAsn.....PheSerValSerI 34
                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.25 (EPA) CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product= "mature PDGF-B chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps: 11
Percent Identity: 34.711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Align seg 1/1 to: US-08-387-845-3 from: 1 to: 868
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US-09-457-066-2_COPY_226_345 x US-08-387-845-3
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                                                                                                                                                                                                      APPLICATION NUMBER: US/08/387,845 FILING DATE:
                                   OPERATING SYSTEM: PC-DOS/MS-DOS
Sequence 3, Application US/08387845
Patent No. 5665567
                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS: LENGTH: 868 base pairs TYPE: nucleic acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Weich, H. A.
Sebald, W.
Schairer, H. U.
Hoppe, U.
FEBS Lett.
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1.636
54.545
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION: 40.762
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
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OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                                                linear
                              GENERAL INFORMATION:
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Ratio:
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                                                                                                                                                                                                                                                                                                                                  TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AUTHORS:
AUTHORS:
JOURNAL:
VOLUME:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; DATE: 1;
US-08-387-845-3
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AUTHORS:
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precursor sequence"
/note= "human PDGF-B gene from pGEM2-PDGF-B,
flanked by 5'-EcoRI und 3'-HindIII
restriction cleavage sites"
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                                                                                                                                                                                                                                                                                                                                  .....TGCTGC....AA 443
                                                                                                                               ......CAGCTGCGACCTGTCCAGGTGAGAAGATCGAGATTGTGCGG 519
                                                                                                                                                                                                                                                                                                           93 ... ArgGlyLeuHisLysSerLeuThrAspValAlaLeuGluHisHisGl 108
49 CysLeuLeuValLysArgCysGlyGlyAsnCysAlaCysCysLeuHisAs 65
                                                                                                                                                                                                        ......LysThrGlyVal.... 92
                                                                                                     nCysAsnGluCysGlnCysValProSerLysValThrLysLysTyrHisG 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.25 (EPA) CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/778,275
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLONE: pMVW-2 (Weich et al., 1986)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
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Patent No. 5935819
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 16
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Schairer, H. U.
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TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Homo sapiens IMMEDIATE SOURCE:
                                                                                                                                                                                                     82 luValLeuGlnLeuArgPro.
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LOCATION: 283..609
OTHER INFORMATION: /pr
PUBLICATION INFORMATION:
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344-348

PAGES:

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CLONE:
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                                                                                                                                                                                                                                                                                                                                                                     19 uValArgLeuTyrSerCysThrProArgAsn....PheSerValSerI 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nCysAsnGluCysGlnCysValProSerLysValThrLysLysTyrHisG 82
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Gaps: 11
Percent Identity: 34.711
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US-09-457-066-2_COPY_226_345 x US-08-778-275-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      444 CAACCGCAACGTGCAGTGCCGCCCCACCCAGGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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APPLICATION NUMBER: 08/387,847
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SEQUENCE CHARACTERISTICS:
LENGTH: 868 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                108.00
1.636
54.545
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NUMBER OF SEQUENCES: 2:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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                                                                                                  Quality:
                                                                                                                   Ratio:
Percent Similarity:
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; DATE: 1986
US-08-778-275-3
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/product= "PDGF-B
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flanked by 5'-EcoRI und 3'-HindIII
restriction cleavage sites"
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US-09-457-066-2_COPY_226_345 x US-08-867-352-3
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                       VANCANISM: Homo sapiens IMMEDIATE SOURCE: CIANE.
                                                                                                                                                                                                                                                              NAME/KEY: mat_peptide
LOCATION: 283..609
OTHER INFORMATION: /pr
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54.545
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AUTHORS: Weich, H. A.
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FEBS Lett.
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OTHER INFORMATION:
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OTHER INFORMATION:
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CDNA
                                                                                                                               LOCATION: 40..762 OTHER INFORMATION:
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               ORIGINAL SOURCE:
                                                                                                               NAME/KEY: CDS
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DATE: 1986
                                                                                                                                                                                                                                              FEATURE:
NAME/KEY:
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AUTHORS:
AUTHORS:
JOURNAL:
VOLUME:
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Ratio:
                          Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Ra
STATE: NC
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      49
                                                                                     APPLICATE: Tekamp-olson, Patricia
TITLE OF INVENTION: METHOD FOR EXPRESSION OF HETEROLOGOUS
TITLE OF INVENTION: PROTEINS IN YEAST
NUMBER OF SOUTHCES: 41
CORRESPONDENCE ADDRESS:
ADDRESSEE: Bell Seltzer IP Group of Alston & Bird, LLP
STREET: 3605 Glenwood Ave. Suite 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
NAME/KEY: misc_feature
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OTHER INFORMATION: /standard_name= "PDGF-B presequence"
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LOCATION: /function= "mediates protein
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OTHER INFORMATION: /product= "PDGF-B propeptide"
OTHER INFORMATION: /standard_name= "PDGF-B prosequence"
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transport"
/product= "PDGF-B propeptide"
/standard_name= "PDGF-B prosequence"
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NAME/KEY: mat_peptide
LOCATION: 697..1023
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                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/989,251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: /standard_name= "rhPDGF-B"
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COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
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    sequence 28, Application US/08989251
    setent No. 6017731
         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Spruill, W. Murray
REGISTRATION UNDRER: 32,943
REFRENCE/DOCKET UNDRER: 5784-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919 420 2202
TELEFAX: 919 881 3175
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
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TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                        ZIP: 27622
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy (
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OTHER INFORMATION:
OTHER INFORMATION:
US-08-989-251-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
                                                                                                                                                                                                                                                        Raleigh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                     ns
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY:
                                                                                                                                                                                                                                                                              STATE: NO COUNTRY:
                                                                                                                                                                                                                                 STREET:
CITY: Ra
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EATURE:
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Length:

Quality: 108.00

alignment\_scores:

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APPLICANT: Tekamp-Olson, Patricia
APPLICANT: TEKAMP-Olson, Patricia
TITLE OF INVENTION: METHOD FOR EXPRESSION OF HETEROLOGOUS
TITLE OF INVENTION: PROTEINS IN YEAST
WINMER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
ADDRESSE: Bell Seltzer IP Group of Alston & Bird, LLP
STREET: 3605 Glenwood Ave. Suite 310
                                                                                                                                                                                                                                                                      775 .. CGGCGCCTCATAGACCGCACCAACGCCAACTTCCTGGTGTGGCCGCCC 822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 892 ......CAGCTGCGACCTGTCCAGGTGAGAAGATCGAGATTGTGCGG 933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        93 ...ArgGlyLeuHisLysSerLeuThrAspValAlaLeuGluHisHisGl 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          934 AAGAAGCCAATCTTTAAGAAGGCCACG...GTGACGCTGGAAGACCACCT 980
                                                                                                                                                                                                                               5 GlyArgLysSerArgValValAspLeuAsnLeuLeuThr.....GluGl 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                            34 leArgGluGluLeuLysArgThrAspThrIlePhe.....TrpProGly 48
                                                                                                                                                                                                                                                                                                                                                 19 uValArgLeuTyrSerCysThrProArgAsn.....PheSerValSerI 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CysLeuLeuValLysArgCysGlyGlyAsnCysAlaCysCysLeuHisAs 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        65 nCysAsnGluCysGlnCysValProSerLysValThrLysLysTyrHisG 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      82 luValLeuGlnLeuArgPro.....92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seq_name: /cgn2_6/ptodata/2/ina/6A_COMB.seq:US-09-340-250-28
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                          Percent Identity: 34.711
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ZIP: 27622

CMDPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/340,250
                                                                                alignment_block:
US-09-457-066-2_COPY_226_345 x US-08-989-251-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Spruill, W. Murray
REGISTRATION NUMBER: 32,943
REFERENCE/DOCKET NUMBER: 5784-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             seq_documentation_block:
; Sequence 28, Application US/09340250
; Patent No. 6083723
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA: APPLICATION NUMBER: 08/989,251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
1.636
54.545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      108 uGluCysAspCys 112
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LOCATION: 455..696
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OTHER INFORMATION: /function= "mediates protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19 uValArgLeuTyrSerCysThrProArgAsn.....PheSerValSerI 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             34 leArgGluGluLeuLysArgThrAspThrIlePhe.....TrpProGly 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 65 nCysAsnGluCysGlnCysValProSerLysValThrLysLysTyrHisG 82
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MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "Synthetic chimera"
ORIGINAL SOURCE:
ORGANISM: Homo sapiens/Saccharomyces cerevisiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length: 121
Gaps: 11
Percent Identity: 34.711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Align seg 1/1 to: US-09-340-250-28 from: 1 to: 1320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 alignment_block:
US-09-457-066-2_COPY_226_345 x US-09-340-250-28
TELECOMMUNICATION INFORMATION:
TELEPAN: 919 420 2202
TELEFAX: 919 881 3175
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 1320 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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NAME/KEY: transit_peptide

LOCATION: 1024..179

OTHER INFORMATION: transport

OTHER INFORMATION: /product-

OTHER INFORMATION: /product-

OTHER INFORMATION: /standard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Quality: 108.00
Ratio: 1.636
milarity: 54.545
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Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         alignment_scores:
                                                                                                                                                                                                                                                                                     FEATURE:
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82	82 luValLeuGlnLeuArgProLysThrGlyVal	93
892	892CAGCTGCGACCTGTCCAGGTGAGAAGATCGAGATTGTGCGG 933	933
93	93ArgGlyLeuHisLysSerLeuThrAspValAlaLeuGluHisHisGl 108	108
934	934 AAGAAGCCAATCTTTAAGAAGGCCACGGTGACGCTGGAAGACCACCT 980	980
108	108 uGluCysAspCys 112	
199		

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January 15, 2002, 22:16:38 ; Search time 33.87 Seconds (without alignments) 269.883 Million cell updates/sec
                                                                                                                                                                                                    US-09-457-066-2_COPY_226_345
666
1 AFVEGRKSRVVDLNLLTEEV......DVALEHHEECDCVCRGSTGG 120
                                                                                                                                                                                                                                                                                                                                                                                              219241
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                     219241 seqs, 76174552 residues
                                                                           OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                         BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                       Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                      Title:
Perfect score:
Sequence:
                                                                                                                                                                                                                                                                                           Scoring table:
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                                                                                                                      Run on:
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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries PIR\_68:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	•	æ			SUMMARIES	
Result No.	Score	Query Match	Query Match Length	DB	ID	Description
П	114.5		148	7	D49530	16K vascular endot
7	110	16.5	166	.~1	JN0248	telet-deri
٣	110	16.5	198	7	JS0735	
4	108		241	П	PFHUG2	
S	106	15.9	200	7	151551	
9	106	٠.	215	7	808220	
7	106		226	7	151550	platelet-derived q
8	105	15.8	245	г	TVCTSS	platelet-derived q
6	104.5	15.7	232	N	A41551	vascular endotheli
10	104		196	7	B28964	platelet-derived q
11	104	15.6	197	7	825096	platelet-derived q
12	104	•	211	٦	PFHUG1	platelet-derived q
13	0	15.6	226	7	TVMVSS	PDGF-related trans
14	102.5	15.4	133	7	B49530	vascular endotheli
15	102.5	15.4	190	7	S52130	vascular endotheli
16	102.5	15.4	196	7	A37359	platelet-derived q
17	102.5	15.4	196	7	A48851	platelet-derived g
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19	101.5	15.2	120	7	A33787	vascular endotheli
20	101.5		146	7	S57956	ovine vascular end
21	101.5	15.2	190	~	B40080	vascular endotheli
	97	•	188	~	JC4680	vascular endotheli
23	97	14.6	207	7	JC4679	vascular endotheli
	96.5	•	190	7	A35987	glioma-derived vas
25	95.5	14.3	190	7	B44881	vascular endotheli
26	S.	14.3	214	7	A44881	vascular endotheli
27	94	14.1	225	7	S25097	platelet-derived g
28	94	14.1	241	~	PFMSGB	
29		13.2	271	7	A25669	PDGF-related trans

vascular endotheli mucin 2 precursor,	placental growth f	placental growth f	hypothetical prote	probable laminin a	similar to gibbere	hypothetical prote	laminin - Hydra vu	plexin A - fruit f	laminin alpha-1 ch	metallothionein -	metallothionein ty	metallothionein-li	protein F14N23.5 [	gibberellin-regula
I51295 A43932	A56125	A41236	T23433	T37316	G84522	G96828	S57894	T13937	S18253	JC2420	T07076	T07114	D86236	T00564
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128 3020	158	149	3672	3704	108	167	171	1945	3712	09	82	82	1188	87
12.9	12.0	11.9	11.6	11.6	11.3	11.2	10.8	10.7	10.7	10.7	10.7	10.7	10.7	10.6
86 83.5	80	79.5	77.5	77.5	75.5	74.5	72	71.5	71.5	7.1	7.1	7.1	7.1	70.5
30	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

 RESULT 1 D49530 IGK vascular endothelial growth factor homolog A2R - Orf virus C.Snecies: Orf virus
C:Date: 07-Apr-1994 #sequence_revision 18-Nov-1994 #text_change 08-Oct-1999 C:Accession: D49530
Rilyttle, D.J.; Fraser, K.M.; Fleming, S.B.; Mercer, A.A.; Robinson, A.J. J. Virol. 68, 84-92, 1994
 A;Title: Homologs of vascular endothelial growth factor are encoded by the poxvirus o A;Reference number: A49530; MUID:94076465 A;Contents: NZ7
 A; Accession: D49530 A; Status: preliminary A; Molecule type: DNA
 A;Wesidues: 1-148 <lit> A;Cross-references: GB:S67522; NID:g456900; PIDN:AAB29223.1; PID:g456902 A;Note: sequence extracted from NCBI backbone (NCBIN:141422, NCBIP:141426)</lit>
 Ouery Match 17.2%; Score 114.5; DB 2; Length 148; Best Local Similarity 30.2%; Pred. No. 0.00029; Matches 29; Conservative 19; Mismatches 43; Indels 5; Gaps 3;
 OY 25 CTPRNFSVSIREEL-KRIDTIEWPCCLLVKRCGGNCACCLHNCNECOCVPSKVTKKYHEV 83
Qy 84 LQLRPKTGVR-GLHKSLTDVALEHHEECDCVCRGST 118 ::: : : : : : :   Db 103 TGVSSSGTNSGVSTNLQRISVTEHTKCDCIGRTTT 138
 RESULT 2 JN0248 platelet-derived growth factor chain A3 precursor - rabbit (fragment) C; Species: Oryctolagus cuniculus (domestic rabbit) C; Date: 09-0ct-1992 #sequence_revision 09-0ct-1992 #text_change 27-Juni-1994
 C;Accession: JN0248 R:Nakahara, K.; Nishimura, H.; Kuro-o, M.; Takewaki, S.; Iwase, M.; Ohkubo, A.; Yazak Biochys. Res. Commun. 184, 811-818, 1992 A;Title: Identification of three types of PDGF-A chain gene transcripts in rabbit vas
A;Reference number: JN0248; MUID:92246970 A;Accession: JN0248 A;Molecule type: mRNA A;Residues: 1-166 <nak></nak>
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16.5%; Score 110; DB 2; Length 166; 30.5%; Pred. No. 0.00088;

Query Match Best Local Similarity

ch

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A; Residues: 26-241 (WEI>
A; Cross-references: GB:X03702; NID:g35374; PIDN:CAA27333.1; PID:g35375
R; Antoniades, H.N.; Hunkapiller, M.W.
Science 220, 963-965, 1983
A; Title: Human platelet-derived growth factor (PDGF): amino-terminal amino acid seque A; Reference number: A94271; WUID:83197379
A; Accession: A94271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: DNA
A; Residues: 'Q', '22-241 < 10525.
R; Lu, K.V.; Rohde, M.F.; Thomason, A.R.; Kenney, W.C.; Lu, H.S.
Biochem. J. 309, 411-417, 1995
A; Title: Mistranslation of a TGA termination codon as tryptophan in recombinant plate
A; Reference number: $56115; MUID:95351967
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R;Rao, C.D.; Pech, M.; Robbins, K.C.; Aaronson, S.A.
Mol. Cell. Biol. 8, 284-292, 1988
A;Title: The S' untranslated sequence of the c-sis/platelet-derived growth factor 2 t
A;Reference number: 157635; MUID:88094398
A;Accession: 157635
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: mRNA
A; Residues: 1-241 <RATY-
A; Cross-references: EMBL:X02744; NID:g30246; PIDN:CAA26524.1; PID:g30247
B; Johnsson, A.; Heldin, C.H.; Wasteson, A.; Westermark, B.; Deuel, T.F.; Huang, J.S.;
EMBO J. 3, 921-928, 1984
A; Title: The c-sis gene encodes a precursor of the B chain of platelet-derived growth
A; Reference number: A55030; MUID:84236121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Reference number: A93308; MUID:83244981
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Molecule type: protein
A;Residues: 82-100, °E', 102-104, °C', 106, °C', 108-110 <ANT>
R;Waterfield, M.D.; Scrace, G.T.; Whittle, N.; Stroobant, P.; Johnsson, A.; Wasteson, Mature 304, 35-39, 1983
A;Title: Platelet-derived growth factor is structurally related to the putative trans
                                                                                                                                                                                                                                            A;Accession: A93366
A;Molecule type: mRNA
A;Residues: 1-21 <COL>
A;COL>
A;COSS-references: GB:X02811; NID:g35371; PIDN:CAA26579.1; PID:g35372
A;Cross-references: GB:X02811; NID:g35371; HOppe, J.
R;Welch, H.A.; Sebald, W.; Schairer, H.U.; Hoppe, J.
FEBS Lett. 198, 344-348, 1986
A;Title: The human osteosarcoma cell line U-2 OS expresses a 3.8 kilobase mRNA which A;Reference number: A25141; MUID:86164981
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Title: Human proto-oncogene nucleotide sequences corresponding to the transforming A; Reference number: A43499; MUID:84097555
A; Accession: A43499
                         A)Cross-references: GB:M12783; GB:M16288; NID:9338210; PIDN:AAA60553.1; PID:9338211 R;Collins, T.; Ginsburg, D.; Boss, J.M.; Orkin, S.H.; Pober, J.S. Nature 316, 748-750, 1985 A;Title: Cultured human endothelial cells express platelet-derived growth factor B A;Reference number: A93366; MUID:85296313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    transforming human c-sis cDNA clones with homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: GB M19719; NID:g189727; PIDN:AAA60349.1; PID:g553608
R;Ratner, L.; Josephs, S.F.; Jarrett, R.; Reitz, M.S.
Nucleic Acids Res. 13, 5007-5018, 1985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Гт,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: protein
A; Mesidues: 82-112 < WATP
R; JOsephs; S.F.; Guo. C.; Ratner, L.; Wong-Staal,
Science 223, 487-491, 1984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Title: Nucleotide sequence of transformi
A;Reference number: 137266; MUID:85269623
A;Accession: 137266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-20 <RAO2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Status: translated from GB/EMBL/DDBJ
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A; Residues: 1-241 <RAO1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Status: preliminary
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A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Accession: A25141
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PFHUGZ
platelet-derived growth factor chain B precursor [validated] - human
N;Alternate names: PDGF B-chain; PDGF-B; PDGF-II; PDGF-related transforming protein (signaterial growth factor chain; PDGF-B; PDGF-II; PDGF-related transforming protein (signaterial growth sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Bodge-Evelsion 20-Sep-1984 #text_change 08-Dec-2000
C;Accession: A94276; A21024; A23532; A93366; A25141; A94771; A93308; A44999; S56115; I57
R;Josephs, S.F.; Ratner, L.; Clarke, M.F.; Westin, E.H.; Reitz, M.S.; Wong-Staal, F.
Science 225, 636-639, 1984
A;Title: Transforming potential of human c-sis nucleotide sequences encoding platelet-de A;Residues: 1-241 a0051>
A;Molecule type: DNA
A;Residues: 1-241 a0051>
A;Molecule sequence analysis identifies the human c-sis proto-oncogene as a str
A;Reference number: A21024; MUID:84205633
A;Accession: A21024
A;Title: Nucleotide sequence analysis identifies the human c-sis proto-oncogene as a str
A;Reference number: A21024
A;Anolecule type: DNA
A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         parelet derived growth factor chain Al precursor - rabbit.
C;Species: oryctolagus cuniculus (domestic rabbit)
C;Species: oryctolagus cuniculus (domestic rabbit)
C;Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 27-Jun-1994
C;Accession: JS0735
R;Nakahara, K.; Nishimura, H.; Kuro-o, M.; Takewaki, S.; Iwase, M.; Ohkubo, A.; Yazaki, Biochem: Biochys: Res. Commun. 184, 811-818, 1992
A;Title: Identification of three types of POGF-A chain gene transcripts in rabbit vascul A;Reference number: JN0248; MUID:92246970
A;Reference number: JN0248; MUID:92246970
A;Residues: 1-198 <NAK>
A;Molecule type: mRNA
A;Residues: 1-198 <NAK>
A;Note: this protein corresponds to the endothelial type of human A chain
C;Superfamily: platelet-derived growth factor
C;Superfamily: platelet-derived growth factor
F;1-20/Domain: signal sequence #status predicted <NRO>
F;21-89/Domain: propeptide #status predicted <PRO>
F;90-198/Product: platelet-derived growth factor Al chain #status predicted <MAT>
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A;Cross-references: GB:RO1917; NID:9338197
Broc. D.; Igarashi, H.; Chiu, I.M.; Robbins, K.C.; Aaronson, S.A.
Proc. Natl. Acad. Sci. U.S.A. 83, 2392-2396, 1986
A;Title: Structure and sequence of the human c-sis/platelet-derived growth factor 2 (SIS A;Reference number: A23532; MUID:86205961
7;
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                                                                             RKSRVVDLNLLTEEVRLYSCTPRNFSVSI - REELKRTDTIF - - WPGCLLVKRCGGNCACC 62
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                                                                                                                                                                                                                                                                                                LHNCNECQCVPSKVTKKYHEVLQLRPKTGVRGLHKSLTDVALEHHEECDCVCRGSTGG 120
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48;
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Mismatches
16;
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Conservative
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Best Local Similarity
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36;
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C:Species: Xenopus lacvis (African clawed frog)
C:Species: Xenopus lacvis (African clawed frog)
C:Species: Xenopus lacvis (African clawed frog)
C:Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 16-Jul-1999
C:Accession: S08220
R:Bejcek, B.E.; Li, D.Y.; Deuel, T.F.
Nucleic Acids Res. 18, 680, 1990
A;Title: Nucleotide sequence of a cDNA clone of Xenopus platelet-derived growth facto
A;Reference number: S08220; MUID:90175018
A;Title: Nucleotide sequence of a cDNA clone of Xenopus platelet-derived growth facto
A;Reference number: S08220; MUID:90175018
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-215 < kBL)
A;Cross-references: EMBL:X17545; NID:964973; PIDN:CAA35583.1; PID:964974
C;Superfamily: platelet-derived growth factor
C;Reywords: alternative splicing; growth factor
C;Reywords: alternative splicing; growth factor
C;Reywords: alternative splicing predicted <SIG>F;23-91,Domain: signal sequence #status predicted <CRO>F;23-91,Domain: propeptide #status predicted <CRO>F;23-91,Domain: propeptide #status predicted <ARD>F;23-91,Domain: propeptide #status predicted <ARD>F;23-91,Domain: properties Predicted <ARD>F;23-91,Domain: properties Predicted <ARD>F;23-91,Domain: Platelet-derived growth factor chain A #status Predi
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C:Species: Xenopus laevis (African clawed frog)
C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 16-Jul-1999
C:Accession: 151550
R:Mercola, M.; Melton, D.A.; Stiles, C.D.
Science 241, 1223-1225, 1988
A:Title: Platelet-derived growth factor A chain is maternally encoded in Xenopus embra A:Reference number: 151550; MUID:88321676
A:Reference number: 151550
A:Status: preliminary; translated from GB/EMBL/DDBJ
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                            A;Cross-references: GB:M23238; NID:g214650; PIDN:AAA49928.1; PID:g214651
C;Superfamily: platelet-derived growth factor
                                                                                                                                                                                                                                                                                                                                         RKSRVVDLULLTEEVRLYSCTPRNFSVSI-REELKRTDTIF--WPGCLLVKRCGGNCACC
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0.0028;
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30.6%; Pred. No. 0.00
tive 15; Mismatches
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A:Residues: 'SISL',17-20,'RQ',22-241 < JOHS-
A:Cross-references: GBX.00559; GBX.00550; GBX.00561; GBX.00562
R:DIKKS, R.P. H.; Onneklnk, C.; Jansen, H.J.; de Jong, A.; Bloemers, H.P.J.
Nucleic Acids Ress. 23, 2815-2829. 1995
A:Arcssion: SB883
A:Arctus; Prefature: Default and and and an archive a promoter in c-sis intron
A:Accession: SB883
A:Actus; Prefature; Prefature a promoter in c-sis intron
A:Accession: SB883
A:Actus; Prefature; Prefature a promoter in c-sis intron
A:Arctus; Prefature; P
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C; Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 16-Jul-1999
C; Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 16-Jul-1999
C; Accession: 151551
Science 241, 1223-1225, 1988
A; Title: Platelet-derived growth factor A chain is maternally encoded in Xenopus embryos A; Reference number: 151550; MUID: 88321676
A; Accession: 151551
A; Accession: 151551
A; Molecule type: mRNA
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Matches 42; Conserv
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Residues: 1-200 <MER>
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A; Molecule type: mRNA

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A,Cross references: GB:S85192; NID:g246155; PID:g246156
A,Accession: C41551
A,Status: nucleic acid sequence not shown
A,Wolecule type: mRNA
A,Residues: 1-140,'N',183-232 <HOU2>
A,Status: nucleic acid sequence not shown; not compared with conceptual translation
A,Wolecule type: mRNA
A,Status: nucleic acid sequence not shown; not compared with conceptual translation
A,Wolecule type: mRNA
A,Residues: 1-141,227-232 <HOU3
R,Tischer, E.; Mitchell, R.; Hartman, T.; Silva, M.; Gospodarowicz, D.; Fiddes, J.C.;
J, Biol. Chem. 266, 11947-11954, 1991
A,Title: The human gene for vascular endothelial growth factor. Multiple protein form
A,Reference number: A40454; MUID:91268072
A,Accession: A40454
A,Molecule type: DNA
A,Residues: 1-165,183-232 <TIL>A,TILS
A,Cross-references: GB:M63971; GB:M63973; GB:M63974; GB:M63975; GB:M63976;
A,Accession: B40454
A,Molecule type: DNA
A,Ressidues: 1-165,183-232 <TIL>A,Cross-references: GB:M63971; GB:M63973; GB:M63974; GB:M63975; GB:M63976;
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A; Residues: 1-140, N', 183-232 < LED>
A; Cross-references: GB:M32977; NID:G181970; PIDN:AAA35789.1; PID:G181971
B; Meindel, K.; Marme, D.; Weich, H.A.
Biochem. Biophys. Res. Commun. 183, 1167-1174, 1992
A; Title: AIDS-associated Kaposi's sarcoma cells in culture express vascular endotheli A; Reference number: JQ1463; MUID:92231879
A; Accession: JQ1463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: DNA
A; Residues: 1-141,227-32 <TI3>
A; Residues: 1-141,227-32 <TI3>
A; Residues: 1-141,227-32 <TI3>
A; Residues: 1-141,227-32 <TI3>
B; Redx, P.J.; Hauser, S.D.; Krivi, G.; Sanzo, K.; Warren, T.; Feder, J.; Connolly, D. Science 246, J309-1312, 1989
A; Title: Vascular permeability factor, an endothelial cell mitogen related to PDGF.
A; Reference number: A40079; MUID:90069609
A; Reference number: A40079

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C;Reywords: alternative splicing; angiogenesis; dimer; disulfide bond; extracellular
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A;Residues: 27-36;43-49, 'R';72-76,'Q',78-81;59-71 <CON>
C;Comment: The most common of several alternatively spliced forms is VEGF 165.
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R;Leung, D.W.; Cachianes, G.; Kuang, W.J.; Goeddel, D.V.; Ferrara, N.
Science 246, 1306-1309, 1989
A;Title: Vascular endothelial growth factor is a secreted angiogenic mitogen.
A;Reference number: A40080; MUID:90069608
A;Accession: A40080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Molecule type: DNA
A;Residues: 1-140,'N',183-232 <TI2>
A;Cross-references: GB:M63971; GB:M63972; GB:M63973; GB:M63974; GB:M63975;
A;Accession: C40454
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A; Residues: 1-140, N', 227-332 cWE2>
A; Residues: 1-140, N', 227-332 cWE2>
A; Experimental Source: ADS-Kaposl's sarcoma cell
B; Connolly, D.T.; Olander, J.V.; Heuvelman, D.; Nelson, R.; Monsell, R.;
J. Biol. Chem. 264, 20017-20024, 1989
A; Title: Hunan vascular permeability factor. Isolation from U937 cells.
A; Reference number: A34492; MUID:90062112
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A;Residues: 1-140,'N',183-232 <WEI>
A;Cross-references: EMBL:X62568; NID:g37658; PIDN:CAA44447.1; PID:g37659
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N.Alternate names: PDGF-related transforming protein
C.Species: Fells silvestris catus (domestic cat)
C.Species: Fells silvestris catus (domestic cat)
C.Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 31-Mar-1996
C.Accession: A26402
R.Yun den Ouweland, A.M.W.; Van Groningen, J.J.M.; Schalken, J.A.; Van Neck, H.W.; Bloem, Nucleic Acids Res. 15, 959-970, 1987
A.Fitle: Genetic organization of the c-sis transcription unit.
A.Recence number: A26402; MUID:87146463
A.Molecule type: mRNA
A.Receidues: 1-245 <VAN>
C.Genetics:
A.Gene: sis
C.Genetics:
A.Gene: sis
C.Superfamily: platelet-derived growth factor
C.Keywords: glycoprotein; growth factor; platelet; proto-oncogene; transforming protein
F.1-20/Domain: signal sequence #status predicted <SIG>F.1-20/Domain: propeptide #status predicted <PRO>F.82-194/Product: platelet-derived growth factor chain B #status predicted
F.32-194/Product: platelet-derived growth factor chain B #status predicted
F.32-157/Region: receptor binding #status predicted
F.53/Binding site: carbohydrate (Asn) (covalent) #status predicted
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N'Alternate names: vascular permeability factor
N'Alternate names: vascular permeability factor
C'Scottains: vascular endothelial growth factor 121 (VEGF 121); VEGF 165; VEGF 189; VEGF C'Scoties: Homo sapiens (man)
C'Date: 28-Aug-1992 #sequence_revision 28-Aug-1992 #text_change 05-Nov-1999
C'Accession: A41551; C41551; B41551; A40454; B40454; C40454; A40079; A40080; J01463; JQ1 R; Houck, K.A.; Ferrara, N.; Winer, J.; Cachianes, G.; Li, B.; Leung, D.W.
Mol. Endocrinol. 5, 1806-1814, 1991
A; Title: The vascular endothelial growth factor family: identification of a fourth molect A; Reference number: A41551; MUID:92168017
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                                                                                                                                                                                                                                                                                                                                                                                                                                         6 RKSRVVDLNLLTEEVRLYSCTPRNFSVSI-REELKRTDTIF--WPGCLLVKRCGGNCACC 62
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                                             A;Cross-references: GB:M23237; NID:g214648; PIDN:AAA49927.1; PID:g214649 C;Superfamily: platelet-derived growth factor
                                                                                                                                                                                                                                                                                                                                               32;
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                                                                                                                                                                                                                                           Query Match 15.9%; Score 106; DB 2; L
Best Local Similarity 30.6%; Pred. No. 0.0029;
Matches 38; Conservative 15; Mismatches 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15.8%; Score 105; DB 1; 33.0%; Pred. No. 0.0039; ive 13; Mismatches 36
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Best Local Similarity
A; Residues: 1-226 <MER>
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GB: M63977

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A; Molecule type: mRNA
A; Residues: 1-197 < HERL>
A; Residues: 1-197 < HERL>
A; Cross-references: ERBL: Z14120; NID:956865; PIDN:CAA78490.1; PID:956866
B; Herren, B.; Weyer, K.A.; Rouge, M.; Loetscher, P.; Pech, M.
Biochim. Biophys. Acta 1173, 294-302, 1993
A; Title: Conservation in sequence and affinity of human and rodent PDGF ligands and rA; Reference number: S33764; MUID:93305723
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Biochim. Biophys. Acta 1222; 511-514, 1994
A;Title: Gene regulation by the 5'-untranslated region of the platelet-derived growth A;Reference number: S47564; MUID:94312450
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A; Residues: 1-21 <TAK>
R; Bonthron, D.; Collins, T.; Grzeschik, K.H.; van Roy, N.; Speleman, F.
Genomics 13, 257-263, 1992
A; Title: Platelet-derived growth factor A chain: confirmation of localization of PDGF
A; Reference number: A42002; MUID:92307656
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                                                                                                                                                              C;Accession: $225096; $33764
R;Herren, B.; Weyer, K.A.; Rouge, M.; Loetscher, P.; Pech, M.
submitted to the EMBL Data Library, July 1992
A;Description: Cross-species conservation in sequence and function of PDGF ligands A;Reference number: $25096
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              platelet-derived growth factor chain A precursor - human N;Alternate names: PDGF A-chain; PDGF-1; PDGF-A; platelet-derived growth factor C;Species: Homo sapiens (man) C;Dete: 04-Dec-1986 #sequence_revision 04-Dec-1986 #text_change 18-Feb-2000 C;Accession: A28964; S47564; A42002; A01379; S00173; A28122 R;Bonthron, D.T.; Morton, C.C.; Orkin, S.H.; Collins, T. Proc. Natl. Acad. Sci. U.S.A. 85, 1492-1496, 1988 A;Title: Platelet-derived growth factor A chain: gene structure, chromosomal loca A;Reference number: A28964; MUID:88144463
                                                                     platelet-derived growth factor chain A precursor - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change 16-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      89 CKTRTVIYEIPRSQVDPTSANFLIWPPCVEVKRCTG---CC--NTSSVKCQPSRVHHRSV 143
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 197;
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0.004;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 104;
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Nature 320, 695-699, 1986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15.6%;
34.0%;
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A;Cross_references: EMBL:Z14120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 15.6
Best Local Similarity 34.0
Matches 32; Conservative
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A, Molecule type: DNA
A, Residues: 1-211 <BON>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: mRNA
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                                                                                                                                                                                                                                                                                                                               A; Accession: S25096
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A; Residues: 152-196 < BO2>
A; Residues: 152-196 < BO2>
Mol. Cell. Biol. 8, 571-577, 1988
A; Title: Structural characterization of the human platelet-derived growth factor A-chain
F;1-232/Product: vascular endothelial growth factor 206 precursor #status predicted <v26 F;1-165,183-232/Product: vascular endothelial growth factor 189 precursor #status predic F;1-141,27232/Product: vascular endothelial growth factor 121 precursor #status predic F;1-26/Domain: signal sequence #status predicted <sIG> F;102/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ВE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Diatelet-derived growth factor chain A precursor splice form 2 - human C; Species: Homo sapiens (man)
C; Accession: B28964; B42002; B28122
R; Bonthron, D.T.; Morton, C.C.; Orkin, S.H.; Collins, T.
FPTOC. NAIL. Acad. Sci. U.S.A. 85, 1492-1496, 1988
A; Title: Platelet-derived growth factor A chain: gene structure, chromosomal location, A; Reference number: A28964; MUID:88144463
A; Accession: B28964
A; Molecule type: DNA
A; Residues: 1-196 < ABN>
A; Residues: 1-196 < ABN>
A; Cross-references: GB:M21571; GB:J03638; GB:M19984; GB:M19985; GB:M19986; GB:M19987; GI
B; Bonthron, D.; Collins, T.; Grzeschik, K.H.; van Roy, N.; Speleman, F.
Genomics 13, 257-263, 1992
A; Title: Platelet-derived growth factor A chain: confirmation of localization of PDGFA A; R; Reference number: A42002; MUID:92307656
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Map position: 7p22-7p22
C;Superfamily: platelet-derived growth factor
C;Reywords: alternative splicing: glycoprotein; growth factor; mitogen; platelet
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                                                                                                                                                                                                                                                                                                                                                                                                 CTPRNFSVSIREEL-KRIDTIFWPGCLLVKRCGGNCACCLHNCNECQCVPSKVTKKYHEV 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CTPRNFSVSI-REELKRIDTIF--WPGCLLVKRCGGNCACCLHNCNECQCVPSKV---TK 78
                                                                                                                                                                                                                                Length 232;
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A;Status: preliminary; not compared with conceptual translation
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                                                                                                                                                                                                                            15.7%; Score 104.5; DB 3
llarity 27.0%; Pred. No. 0.0042;
Conservative 21; Mismatches 33
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A; Cross-references: GB:M20488
A; Note: the authors translated the
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24; Conserv
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Matches 32;
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Best Local S:
Matches 24
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Indels

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M.S.;

P.; Urdea,

chromosomal location

Gaps

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Vascular endothelial growth factor - pig
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 14-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 05-Nov-1999
C;Accession: S52130
R;Sharma, H.S.; Tang, Z.H.; Gho, B.C.G.; Verdouw, P.D.
Biochim: Biophys. Acta 1260, 235-238, 1995
A;Title: Nucleotide sequence and expression of the porcine vascular endothelial growt
A;Reference number: S52130; MUID:95143284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Species: Orf virus
C;Date: 07-Apr-1994 #Sequence_revision 18-Nov-1994 #text_change 08-Oct-1999
C;Accession: B45330
R;Lyttle, D.J.; Fraser, K.M.; Fleming, S.B.; Mercer, A.A.; Robinson, A.J.
J. Virol. 68, 84-92, 1994
A;Fitle: Homologs of vascular endothelial growth factor are encoded by the p.A;Reference number: A49530; MUID:94076465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       73 VAEPAMIAECKTRTEVFEIS-RRLIDRTNANFLVWPPCVEVQRCSG---CC--NNRNVQC 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: GB:S67520; NID:9456897; PIDN:AAB29220.1; PID:9456899 A;Note: sequence inconsistent with nucleotide translation A;Note: sequence extracted from NCBI backbone (NCBIN:141426)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16 LTEEVRLYSCTPRN--FSVSIREELKRTDTIF--WPGCLLVKRCGGNCACCLHNCNECQC 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17 TEEVRLYSCTPRNFSVSIRE---ELKRTDTIFWPGCLLVKRCGGNCACCLHNCNECQCVP 73
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Residues: 1-190 <SHA>
A;Cross-references: GB:X81380; NID:9587559; PIDN:CAA57143.1; PID:9587560
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                                                                                                                               C;Keywords: growth factor; transforming protein F;6-226/Domain: platelet-derived growth factor chain B similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         vascular endothelial growth factor homolog A2R, 14.7K - Orf virus
                                                                                                                                                                                                                                                                                                              Length 226;
                                                                                                                                                                                                                                                                                                                                                                                                             34; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 72 VPSKVTKKYHEVLQLRP----KTGV----RGLHKSLTDVALEHHEECDC 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           127 RPTQV-,-----QLRPVQVRKIEIVRKKPIFKKAT-VTLEDHLACKC 165
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15.4%; Score 102.5; DB 2; 27.0%; Pred. No. 0.0055; tive 20; Mismatches 34;
                                                                                                                                                                                                                                                                                                     15.6%; Score 104; DB 1; 33.3%; Pred. No. 0.0046; iive 12; Mismatches 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15.4%; Score 102.5; DB 30.5%; Pred. No. 0.004;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18; Mismatches
                                                                                     growth factor
                                                                                     C; Superfamily: .platelet-derived
                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 33.38
Matches 36; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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Best Local Similarity
Matches 32; Conservat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-133 <LYT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 24; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Accession: B49530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Contents: NZ2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14
                                          A; Gene:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Dβ
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A.Reference number: A01379; MUID:86203630
A.Reference number: A01379; MUID:86203630
A.Rolecule type: mRNA
A.Rolecule type: mRNA
A.Rolecule type: mRNA
A.Cross references: GB:X03795; NID:935365; PIDN:CAA2741.1; PID:935366
A.Cross references: GB:X03795; NID:935365; PIDN:CAA2741.1; PID:935366
A.Title: The long 3'-untranslated regions of the PDGF-A and -B mRNAs are only distantly A.Rocession: S00173
A.Rolecule type: mRNA
A.Reference number: S00173; MUID:88030061 of the PDGF-A and -B mRNAs are only distantly A.Rocession: S00173
A.Rocession: S00173
A.Rocession: S00173
A.Rolecule type: mRNA
A.Ro
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N.Alternate names: p28-sis
N.Alternate names: p28-sis
C.Species: sinian sarcoma virus
C.Species: sinian sarcoma virus
C.Species: 23-Jul-1983 #sequence_revision 20-Sep-1984 #text_change 31-Oct-1997
C.Shecession: A01381
R.Devare, S.G.; Reddy, E.P.; Law, J.D.; Robbins, K.C.; Aaronson, S.A.
Proc. Natl. Acady, E.P.; Law, J.D.; Robbins, K.C.; Aaronson, S.A.
A.Title: Nucleotide sequence of the simian sarcoma virus genome: demonstration that its
A.Reference number: A03982; MuID:83144004
A.Reference number: A03982; MuID:83144004
A.Residues: 1-226 CDEV>
C.Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               79 KYHEVLQLRPKTGVRGLHKSLTDVALEHHEECDC 112
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<sup>84</sup> LOLRPKTGVRGLHKSLTDVALEHHEECDC 112 :::: | :|: | 1:| 106 MRIKPHQG-----QHIGEMSFLQHNKCEC 129

Search completed: January 15, 2002, 22:17:35 Job time: 57 sec

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January 15, 2002, 22:20:38 ; Search time 24.01 Seconds
(without alignments)
183.248 Million cell updates/sec
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11 AFVFGRKSRVVDL/NLL/TEEV......DVALEHHEECDCVCRGSTGG 120
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Gapop 10.0 , Gapext 0.5
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SwissProt\_39:\*

Database :

Description	P52885 orf virus (P34007 oryctolagus P26617 cavia porce P01127 homo sapien P13698 xenopus lae P49765 homo sapien P20919 felis slive P15692 homo sapien P2093 mus musculu P01128 simian sarc P5284 orf virus (P49151 sus Scrofa P49767 homo sapien P50128 simian sarc P5284 orf virus (P49151 sus scrofa P49767 homo sapien P50128 mus musculu P16612 rattus norv Q00731 mus musculu P5282 quilus quil Q95289 ovis aries P1240 mus musculu P5282 quilus gall Q9523 ovis aries P49764 mus musculu P5282 quilus quil Q95282 quilus quil Q95282 quilus quil Q95281 parachandi P5284 paqothenia Q93450 parachaenic Q99499 dicentrarch
SUMMARIES	VECH ORENY PDGA_RABIT PDGA_RABIT PDGA_RABIT PDGB_HUMAN PDGGA_XEMIA VEGE HUMAN PDGG_RELCA VEGE HUMAN PDGA_MOUSE TSIS_SMSAV VEGE_PUG VEGC_HUMAN VEGC_HUMAN VEGC_HUMAN VEGC_RAT VEGE_RAT V
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LMB1_HYDAT LMA_DROME MT_OREMO MT_ZOAVI MT3_LVCES ITBX_DROME MT3_HORSE MT3_HORSE MT3_LIZAU MT21_CRYSA SUHW_DROVI DCA2_DIACA	ALIGNMENTS  Created) Last sequence update). Last annotation update) GROWTH FACTOR HOMOLOG PRECUR GROWTH FACTOR HOMOLOG PRECUR ) (OV NZ-7). S. no RNA stage; Poxviridae; SE, DISULFIDE LINKED (BY SIMILY OF STRICT) SE, DISULFIDE SIMILARITY. SE, SECOFELIAL SIMILARITY. SE, SECOFELIAL SE SIMILARITY. SE SIMILARI	6
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RA Makahara K.-I., Nishimura H., Kuro-O M., Takewaki S.-I., Iwase M.,
RA Ohkubo A., Yazaki Y., Magai R.;*.

A Ohkubo A., Yazaki Y., Magai R.;*.

Identification of three types of Pubper of Pubpit vascular smooth muscle and their regulated expression during rabbit vascular smooth muscle and their regulated expression during RT abbit vascular smooth muscle and their regulated expression during RT abboth vascular smooth muscle and their regulated expression during RT abboth vascular smooth muscle snot II.";

B. Gochem. Blophys. Res. Commun. 184:811-818(1992).

C. I- FUNCTION: PLATELET-DERIVED GROWTH FACTOR IS A POTENT MITGEN FOR CELLS OF MESENCHYMAL ORIGIN. BINDING OF THIS GROWTH FACTOR TO ITS AFFINITY RECEPTOR ELICITS A VARIETY OF CELLULAR RESPONSES. IT IS RELEASED BY PLATELETS UPON WOUNDING AND PLAYS AN IMPORTANT ROLE.

IN STIMULATING ADJACENT CELLS TO GROW AND THEREBY HEBL THE WOUND.

C. I- SUBUNIT: ANTIPARALLEL DISULFIDE-LINKED DIMER OF NONIDENTICAL (A AND B) CHAINS. HOMODIMERS OF A AND B CHAINS ARE IMPLICATED IN TRANSFORMATION PROCESSES.

C. I- ALTERNATIVE PRODUCTS: 3 ISOFORMS; A1, A2 (SHOWN HERE) AND A3; ARE PRODUCTS.

PRODUCTS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- INDUCTION: THE FORM A3 IS SELECTIVELY INDUCED BY ANGIOTENSIN II.
-!- MISCELLANEOUS: A'A AND B-B, AS WELL AS A-B, DIMERS CAN BIND TO THE
                        Growth factor; Platelet; Alternative splicing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BY SIMILARITY.

REMOVED BY PROTEOLYSIS (BY SIMILARITY).

PLATELET-DERIVED GROWTH FACTOR, A CHAIN.

RECFPTOR BINDING SITE (POTENTIAL).

BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PDGF RECEPTOR.

-1-SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS.
PIR; JS0735, JS0735.
PIR; PS0340;, PS0387.
PIR; JN0248; JN0248.
                                                                                                                                                                                                                                                    Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
             CTPRNFSVSIREEL-KRTDTIFWPGCLLVKRCGGNCACCLHNCNECQCVPSKVTKKYHEV
                                                                                                                                                                           01-FEB-1994 (Rel. 28, Created)
1-FEB-1994 (Rel. 28, Last sequence update)
20-AGG-2001 (Rel. 40, Last annotation update)
PLATELET-DERIVED GROWTH FACTOR, A CHAIN PRECURSOR (PDGF A-CHAIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-LINKED (GLCNAC. . .) (POTENTIAL).
GRR -> DVR (IN ISOFORM A1).
MISSING (IN ISOFORM A1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INTERCHAIN (BY SIMILARITY).
INTERCHAIN (BY SIMILARITY).
                                                                             103 TGVSSSGTNSGVSTNLQRISVTEHTKCDCIGRTTT 138
                                                              84 LQLRPKTGVR-GLHKSLTDVALEHHEECDCVCRGST 118
                                                                                                                                                     213 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-LINKED
GRR -> DV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HSSP, P01127, 1PDG.
InterPro; IPR002400; GF_cysknot.
InterPro; IPR000072; PDGF.
Pfam; PP00341; PDGF: 1.
                                                                                                                                                                                                                                                                                                                                   TISSUE=Vascular smooth muscle;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SMART; SM00141; PDGF; 1.
PROSITE; PS00249; PDGF_1; 1.
PROSITE; PS50278; PDGF_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS; PR00438; GFCYSKNOT.
ProDom; PD001629; PDGF; 1.
                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20
89
213
1162
1179
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                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                           NCBI_TaxID=9986;
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                                                                                                                                                   PDGA_RABIT
P34007;
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RRRESGKKRKRKRLRPT -> TLLPAPGGCVHPQGCLRAHDG
CQSSRNHMQALGWKKKM (IN ISOFORM A3).
28A9B7E50487F4C5 CRC64; ·
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- SUBUNIT: HOMODIMER; DISULFIDE-LINKED.
-!- SUBCELLULAR LOCATION: SECRETED BUT REMAINS ASSOCIATED TO CELLS OR
TO THE EXTRACELLULAR MATRIX UNLESS RELEASED BY HEPARIN (BY
                                                                                                                                                                                                                                                                 85 RRKRII-----EEAIPAICKTRTVIYEIPRSOVDPTSANFLIWPPCVEVKRCTG---CC 135
                                                                                                                                                                     Gaps
                                                                                                                                                                                                               6 RKSRVVDLNLLTEEVRLYSCTPRNFSVSI-REELKRTDTIF--WPGCLLVKRCGGNCACC 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Berse B.;
Submitted (XXX-1992) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: GROWTH FACTOR ACTIVE IN ANGIOGENESIS, AND ENDOTHELIAL CELL GROWTH. INDUCES ENDOTHELIAL PROLIFERATION AND WASCULAR
                                                                                                                                                                                                                                                                                                             63 LHNCNECQCVPSKVTKKYHEVLQLRPKTGVRGLHKSLTDVALEHHEECDCVCRGSTGG 120
                                                                                                                                                                                                                                                                                                                                           SIMILARITY).
SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
VASCULAR ENDOTHELIAL GROWTH FACTOR (VEGF) (VASCULAR PERMEABILITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (POTENTIAL).
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                                                                                                                    Length 213;
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BY SIMILARITY.
BY SIMILARITY.
INTERCHAIN (BY SIMILARITY).
INTERCHAIN (BY SIMILARITY).
N-LINKED (GLCNAC. . .) (POTEN
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Pred. No. 0.00021;
                                                                                                                 16.5%; Score 110; DB 1; 30.5%; Pred. No. 0.00019; ive 16; Mismatches 48
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PROSITE; PS50278; PGGF_2; 1.
Mitogen; Growth factor; Glycoprotein.
DISULFID 25 67 BY SIMIL
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26.5%;
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                                                 24005
                                                                                                                 Query Match
Best Local Similarity 30.59
Matches 36; Conservative
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                                              213 AA;
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Best Local Similarity
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SEQUENCE
                                                 SEQUENCE
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(OCT-1996) to the EMBL/GenBank/DDBJ databases
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  Gaps
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                        18 EEVRLYS-----CTPRNFSVSIREEL-KRTDTIFWPGCLLVKRCGGNCACCLHNCNECQ 70
                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-86205961; PubMed-3517869; RabCLD., Igarashi H., Chiu I.-M., Robbins K.C., Aaronson S.A.; Rao C.D., Igarashi H., Chiu I.-M., Robbins K.C., Aaronson S.A.; "Structure and sequence of the human c-sis./platelet-derived growth factor 2 (SIS/PDGF2) transcriptional unit."; Proc. Nati. Acad. Sci. U.S.A. 83:2392-2396(1986).
                                      Collins T., Ginsburg D., Boss J.M., Orkin S.H., Pober J.S.; "Cultured human endothelial cells express platelet-derived growth factor B chain: CDNA cloning and structural analysis."; Nature 316:748-750(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ratner L., Josephs S.F., Jarrett R., Reitz M.S., Wong-Staal F.; Nucleotide sequence of transforming human c-sis cDNA clones with homology to platelet-defined growth factor."; Nucleic Acids Res. 13:5007-5018(1985).
                                                                                                                                                                                                                                                              Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=87217119; PubMed=3472769; Rao C., Aaronson S.A.; Rao C.D., Igarashi H., Pech M.W., Robbins K.C., Aaronson S.A.; "Oncogenic potential of the human platelet-derived growth factor transcriptional unit.";
                                                                                                                                                             P01127; P78431;
21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
PLATELET-DERIVED GROWTH FACTOR, B CHAIN PRECURSOR (PDGF B-CHAIN)
(PDGF-2) (C-SIS) (BECAPLERMIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   \epsilon analysis identifies the human c-sis structural gene for platelet-derived growth
  17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 22-241 FROM N.A.
MEDLINE-84205633; PubMed-6327048;
Chiu I.-M., Reddy E.P., Givol D., Robbins K.C., Tronick S.R.,
                                                                                                                                                                                                                                                                                                                    MEDLINE-84250225; PubMed-6740330;
Josephs S.F., Ratner L., Clarke M.F., Westin E.H., Reitz M.S.
  Indels
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                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; E
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                      CVPSKVTKKYHEVLQLRPKTGVRGLHKSLTDVALEHHEECDC 112
                                                                                    |||:: :::::| | :|:|
| CVPTEEFNITMQIMRIKPHQG-----QHIGEMSFLQHSKCEC 103
37;
                                                                                                                                                      241 AA
21; Mismatches
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  Conservative
                                                                                                                                                       STANDARD;
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Burgess J., Odell C.;
                                                                                                                                                                                                                                                  Homo sapiens (Human).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  proto-oncogene as a
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  Matches
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MUTAGENESIS, & IMPORTANCE OF ARG-108 AND ILE-111 FOR RECEPTOR-BINDING. MEDLINE-92097530; PubMed=1661670; Clements J.M., Bawden L.J., Bloxidge R.E., Catlin G., Cook A.L., Craig S., Drummond A.H., Edwards R.M., Fallon A., Green D.R., Hellewell P.G., Kirwin P.M., Nayee P.D., Richardson S.J., Brown D., Chahwala S.B., Snarey M., Winslow D.; Two POGF-B chain residues, arginine 27 and isoleucine 30, mediate receptor binding and activation."; EMBO J. 10:4113-4120(1991).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDINE-83344981. PubMed-6306471;
Waterfield M.D., Scrace G.T., Whittle N., Stroobant P., Johnsson A., Wasteson A., Westermark B., Heldin C.H., Huang J.S., Deuel T.F., "Platelet-derived growth factor is structurally related to the putative transforming protein p28sis of simian sarcoma virus.";
                          MEDLINE=97141927; PubMed=8988177; Simon M.-P., Pedeutour F., Sirvent N., Grosgeorge J., Minoletti F., Coindre J.-M., Terrier-Lacombe M.-J., Mandahl N., Craver R.D., Blin N., Sozzi G., Turc-Carel C., O'Brien K.P., Kedra D., Fransson I., Guilbaud C., Dumanski J.P., Deregulation of the platelet-derived growth factor B-chain gene via fusion with collagen gene COLIA1 in dermatofibrosarcoma protuberans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-83197379; PubMed-6844921;
Antoniades H.N., Hunkapiller M.W.;
"Human platelet-derived growth factor (PDGF): amino-terminal amino
                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 26-241 FROM N.A.
MEDLINE=86164981; PubMed=3456904;
Melch H.A., Sebald W., Schairer H.U., Hoppe J.;
"The human osteosarcoma cell line U-2 OS expresses a 3.8 kilobase mRNA which codes for the sequence of the PDGF-B chain.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Deuel T.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQÜENCE OF 153-200 FROM N.A., AND PARTIAL SEQUENCE. MEDLINE-84236121; Pubmed-6329745; Johnsson A., Heldin C.H., Wasteson A., Westermark B., Huang J.S., Seeburg P.H., Gray A., Ullrich A., Scrace Stroobant P., Waterfield M.D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "The c-sis gene encodes a precursor of the B chain of platelet-derived growth factor.";
EMBO J. 3:921-928(1984).
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                                                                                                                                                                                                                                                                                         and giant-cell fibroblastoma.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lett. 198:344-348(1986).
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SEQUENCE OF 1-53 FROM N.A.
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112 C 112

59 CACCLHNCNECQCVPSKVTKKYHEVLQLRP----KTGV---RGLHKSLTDVALEHHEECD

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                                             MISCELLANEOUS: A-A AND B-B, AS WELL AS A-B, DIMERS CAN BIND TO THE
                     PHARMACEUTICAL: AVAILABLE UNDER THE NAME REGRANEX (ORTHO-MCNEIL). USED TO PROMOTE HEALING IN DIABETIC NEUROPATHIC FOOT ULCERS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PLATELET-DERIVED GROWTH FACTOR, B CHAIN.
                                                                 SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS. DATABASE: NAME=RAD Systems. COM/COYL COURCE DOOK; WWW="http://www.rndsystems.com/coyl_cat/pdgf.html". DATABASE: NAME=Regranex; NOTE=Clinical information on Regranex;
AND B) CHAINS. HOMODIMERS OF A AND B CHAINS ARE IMPLICATED IN TRANSFORMATION PROCESSES.
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BINDING.
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PROSITE; PS50278; PDGF_2; 1.
Mitogen; Growth factor; Proto-oncogene; Platelet; Signal; Pharmaceutical; 3D-structure.
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F -> E (IN REF. 11).

E -> C (IN REF. 11).

S -> C (IN REF. 11).
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                                                                                                               WWW="http://www.regranex.com/"
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InterPro; IPR000072; PDGF.
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ProDom; PD001629; PDGF; 1.
SMART; SM00141; PDGF; 1.
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K01916; AAA98793.1; J
X03702; CAA2733.1; -
Z81010; CAB02635.1;
X00561; CAA25229.1; -
X98706; CAA67262.1; -
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105
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                                                                                                                                                                                                                                                                                                                                                                                                                                               PIR; A94276; PFHUG2.
PDB; 1PDG; 31-JAN-94.
                                                         PDGF RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   82
191
108
1111
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97
130
134
134
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101
105
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                                                                                                                                                                                                                                                                        K01399;
K01400;
                                                                                                                                                                                                                                         K01918;
                                                                                                                                                                                                                                                 J00121;
                                                                                                                                                                                                                                                              K01398;
                                                                                                                                                                                                                                                                                                                                K01917;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MIM; 190040;
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CONFLICT
CONFLICT
CONFLICT
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                                                                                                                                                                                                                                                                                               EMBL;
EMBL;
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                                                                                                                                                                                                                                                                                                                                           EMBL;
EMBL;
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EMBL;
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EMBL;
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                                                                                                                                                                                                                                                                          EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MISCELLANBOUS: A-A AND B-B, AS WELL AS A-B, DIMERS CAN BIND TO THE PDGF RECEPTOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUCLEIC ACIDS RES. 18:60-680(1990).

**INCTION: PLATELET-DERIVED GROWTH FACTOR IS A POTENT MITOGEN FOR CELLS OF MESEMCHYMAL ORIGIN. BINDING OF THIS GROWTH FACTOR TO ITS AFFINITY RECEPTOR TO ITS AFFINITY RECEPTOR ELICITS A VARIETY OF CELLULAR RESPONSES. IT IS RELEASED BY PLATELETS UPON WOUNDING AND PLAYS AN IMPORTANT ROLE IN STIMULATING ADJACENT CELLS TO GROW AND THEREBY HEAL THE WOUND.

**INCHINATION ANTIPARALLEL DISULFIDE-LINKED DIMER OF NONIDENTICAL (A AND B) CHAINS. HOMODIMERS OF A AND B CHAINS ARE IMPLICATED IN TRANSFORMATION PROCESSES.

**INCHINATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN HERE) AND A SHORT FORM; ARE PRODUCED BY ALTERNATIVE SPLICING. THE LONG FORM CONTAINS A BASIC INSERT WHICH ACTS AS A CELL RETENTION SIGNAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS.
                                                                                                                                                                                                                                                               Eukaryota, Metazoa, Chordata, Craníata, Vertebrata, Euteleostomi,
Amphibia; Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-88321676; PubMed-3413486;
Mercola M., Melton D.A., Stiles C.D.;
"Platelet-derived growth factor A chain is maternally encoded in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bejock B.E., Li D.Y., Deuel T.F., "Nucleotide sequence of a cDNA clone of Xenopus platelet-derived
                                                                                                                                         01-JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
PLATELET-DERIVED GROWTH PACTOR, A CHAIN PRECURSOR (PDGF A-CHAIN)
                                                                                                     226 AA
                                                                                                                                                                                                                                              Xenopus laevis (African clawed frog).
                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; M23237; AAA49927.1; --
EMBL; M23238; AAA4928.1; --
EMBL; X17545; CAA35583.1; --
PIR; S08220; S08220.
HSSP; P01127; 1PBG.
InterPro; IPR002400; GC_cysknot.
InterPro; IPR000072; PDGF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=00cyte;
MEDLINE=90175018; PubMed=2308861;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Xenopus embryos.";
Science 241:1223-1225(1988).
                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  growth factor A-chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00341; PDGF; 1.
                                                                                                                                                                                                                                                                                                           Xenopus.
                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=8355
                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=Oocyte;
                                                                                                                                                                                                                                                                                                         xenopodinae;
                                                                                                   PDGA_XENLA
Ċ 180
                                                                                                                                                                                                                            (PDGFA)
                                                                              PDGA_XENLA
  180
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11;

Gaps

32;

35; Indels

Mismatches

12;

Conservative

42;

Best Loc Matches

Similarity

Local

Query Match

Length 241;

; DB 1; 0.00035;

Score 108; Pred. No. 0

16.2%; 34.7%;

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HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CHAIN
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 QQ
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20-AUG-2001 (Rel. 40, Last annotation update)
VASCULAR ENDOTHELIAL GROWTH FACTOR B PRECURSOR (VEGF-B) (VEGF RELATED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS00249; PDGF_1; 1.
PROSITE; PS50278; PDGF_2; 1.
Glycoprotein; Mitogen; Growth factor; Platelet; Alternative splicing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     63 LHNCNECQCVPSKVTKKYH-----EVLQLRPKTGVRGLHKSLTDVALEHHEECDCVC 114
                                                                                                                                                 REMOVED BY PROTEOLYSIS.
PLATELET-DERIVED GROWTH FACTOR, A CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Cloning and characterization of a novel human gene related to vascular endothelial growth factor."; Genome Res. 6:124-131(1996).
-i. FUNCTION: GROWTH FACTOR FOR ENDOTHELIAL CELLS. BINDS HEPARIN.
-i. SUBUNIT: HOMODIMER; DISULFIDE-LINKED. CAN ALSO FORM HETERODIMER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDILINE=97077124; PubMed=8919691;
Grimmond S., Lagercrantz J., Drinkwater C., Silins G., Townson S.,
Pollock P., Gotley D., Carson E., Rakar S., Nordenskjoeld M., Ward
Hayward N., Weber G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RKSRVVDLNLLTEEVRLYSCTPRNFSVSI-REELKRTDTIF--WPGCLLVKRCGGNCACC
                                                                                                                                                                                                                                        INTERCHAIN (BY SIMILARITY).
INTERCHAIN (BY SIMILARITY).
N-LINKED (GLCNAC. . ) (PROBABLE).
GFF -> DVR (IN SHORT ISOFORM).
MISSING (IN SHORT ISOFORM).
MISSING (IN REF. 2).
Q -> R (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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U.;
for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Olofsson B., Pajusola K., Kaipainen A., von Euler G., Joukov Saksela O., Orpana A., Pettersson R.F., Alitalo K., Eriksson "Vascular endothelial growth factor B, a novel growth factor
                                                                                                                                                                                                                                                                                                                                                                                                                                     15.9%; Score 106; DB 1; Length 226; 30.6%; Pred. No. 0.00053;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          39; Indels
                                                                                                                                                                                                                                                                                                                                                          -> R (ÎN REF. 2).
E3E724FCF67C2FB2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       endothelial cells.";
Proc. Natl. Acad. Sci. U.S.A. 93:2576-2581(1996).
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                                                                                                                                                                                         SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15; Mismatches
                                                                                                                                                                                                           SIMILARITY
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MEDLINE=96197355; PubMed=8637916;
                                                                                                                                                                                     BY
BY
BY
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M
PR00438; GFCYSKNOT PD001629; PDGF; 1.
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                                      SM00141; PDGF; 1.
                                                                                                                               22
91
226
145
1145
1184
1139
139
200
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226 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 38; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   187 NSNS 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              115 RGST 118
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P49765;
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CONFLICT
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                     ProDom;
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                                                                                                                               SIGNAL
                                                                                                                                                   PROPEP
                                                                                                              Signal
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                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   van den Ouweland A.M.W.;
Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: PLATELET-DERIVED GROWTH FACTOR IS A POTENT MITOGEN FOR CELLS OF MESENCHYMAL ORIGIN. BINDING OF THIS GROWTH FACTOR TO ITS AFFINITY RECEPTOR ELICITS A VARIETY OF CELLULAR RESPONSES. IT IS RELEASED BY PLATELETS UPON WOUNDING AND PLAYS AN IMPORTANT ROLE
OR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GRKSRVVD-LNLLTEEVRLYSCTPRNFSVSIREELKRT-DTIFWPGCLLVKRCGGNCACC 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBCELLULAR LOCATION: SECRETED BUT REMAINS ASSOCIATED TO CELLS
                        TO THE EXTRACELLULAR MATRIX UNLESS RELEASED BY HEPARIN. TISSUES EMETICITY: EXPRESSED IN ALL TISSUES EMEDT LIVER. HIGHEST LEVELS FOUND IN HEART, SKELETAL MUSCLE AND PANCRESS. SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 pDGFB OR SIS.
Felis silvestris catus (Cat).
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-OCT-1989 (Rel. 12, Last sequence update)
20-MG-2001 (Rel. 40, Last annotation update)
PLATELET-DERIVED GROWH FACTOR, B CHAIN PRECURSOR (PDGF B-CHAIN)
(PDGFB) (C-SIS) (PDGF-2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GROWTH FACTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 188;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63 LHNCNECQCVPSKVTKKYHEVLQLRPKTGVRGLHKSLTDVALEHHEECDC 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PD--DGLECVPTGQHQVRMQILMIRYPS-----SQLGEMSLEEHSQCEC 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  40; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VASCULAR ENDOTHELIAL GROW F04654D5A3727194 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS00249; PDGF_1; 1.
PROSITE; PS50278; PDGF_2; 1.
Mitogen; Growth factor; Signal; Heparin-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 105.5; DB 1 Pred. No. 0.00049;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15.8%; Sco...
28.2%; Pred. No. v...
... 22; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            245 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21261 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; U48801; AAB06274.1; -. EMBL; U43369; AAA91463.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR000072; PDGF. Pfam; PF00341; PDGF; 1. ProDom; PD001629; PDGF; 1. SMART; SM00141; PDGF; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P15692; 1VPF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  188 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MIM; 601398;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31;
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P12919;
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SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local 3
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Science 246:1306-1309(1989).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              mapping of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       binding."
    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8
                                                                                                                                  modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
IN STIMULATING ADJACENT CELLS TO GROW AND THEREDI DEDU LLL DOCUMENT: STRUNTERALLEL DISULFIDE-LINKED DIMER OF NONIDENTICAL (A AND B) CHAINS. HOWOLIMERS OF A AND B CHAINS ARE IMPLICATED IN TRANSFORMATION PROCESSES.

MISCELLANEOUS: A-A AND B-B, AS WELL AS A-B, DIMERS CAN BIND TO THE PDGF RECEPTOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        92 VAEPAMIAECKTRTEVFEVS-RRLIDRTNANFLVWPPCVEVQRCSG---CC--NNRNVQC 145
                                                                                                                                                                                                                                                                                                                                           PLATELET-DERIVED GROWTH FACTOR, B CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16 LTEEVRLYSCTPRN--FSVSIREELKRTDTIF--WPGCLLVKRCGGNCACCLHNCNECQC 71
                                                                   -!- SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=90069608; PubMed=2479986;
Leung D.W., Cachianes G., Kuang W.-J., Goeddel D.V., Ferrara N.;
"Vascular endothelial growth factor is a secreted angiogenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
20-AUG-2001 (Rel. 16) Last annotation update)
VASCULAR ENDOTHELIAL GROWTH FACTOR PRECURSOR (VEGF) (VASCULAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 245;
                                                                                                                                                                                                                                                                                                                                                             BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
INTERCHAIN (BY SIMILARITY).
INTERCHAIN (BY SIMILARITY).
A; E7715291D9837512 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            36; Indels
                                                                                                                                                                                                                                                                                                         Mitogen; Growth factor; Proto-oncogene; Platelet; Signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              72 VPSKVTKKY-----HEVLQLRPKTGVRGLHKSLTDVALEHHEECDC 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15.8%; Score 105; DB 1; 33.0%; Pred. No. 0.00072; iive 13; Mismatches 36;
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                                                                                                                                                                                                                                                                                                                     BY SIMILARITY.
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                                                                                                                                                                                 EMBL; X05112; CAA28758.1; ALT_SEQ.
                                                                                                                                                                                                    HSSP, P01127; 1PDG.
InterPro: IPR002400; GF_Cysknot.
InterPro: IPR000072; PDGF.
Pfam: PF00341; PDGF: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                      27787 MW;
                                                                                                                                                                                                                                                PRINTS; PRO0438; GFCYSKNOT.
Probom; PD001629; PDGF; 1.
SMART; SM01041; PDGF; 1.
PROSITE; PS00249; PDGF_1; 1.
PROSITE; PS50278; PDGF_2; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 15.85
Best Local Similarity 33.05
Matches 35; Conservative
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245
145
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128
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195
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138
128
137
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PROPEP
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VEGF_HUMAN
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Wiesmann C., Christinger H.W., Cochran A.G., Cunningham B.C., Falrbrother W.J., Keenan C.J., Meng G., de Vos A.M.; "Crystal structure of the complex between VEGF and a receptor-blocking nearlide.":
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "AIDS-associated Kaposi's sarcoma cells in culture express vascular endothelial growth factor.",
                                                                                                                                                                    "Vascular permeability factor, an endothelial cell mitogen related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF 34-135.
MEDLINE-97352774; PubMed-9207067;
Muller Y.A., Li B., Christinger H.W., Wells J.A., Cunningham B.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-90062112; PubMed-2584205; Connolly D.T., Olander J.V., Heuvelman D., Nelson R., Monsell R., Siegel N., Haymore B.L., Leingruber R., Feder J.; "Human vascular permeability factor. Isolation from U937 cells."; J. Biol. Chem. 264:20017-20024(1989).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "The human gene for vascular endothelial growth factor. Multiple protein forms are encoded through alternative exon splicing."; J. Biol. Chem. 266:11947-11954(1991).
SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
MEDILINE=90069609; PubMed-2479987;
Keck P.J., Hauser S.D., Krivi G., Sanzo K., Warren T., Feder J.,
Connolly D.T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fiebich B.L., Jaeger B., Schoellmann C., Weindel K., Wilting Rochs G., Marme D., Hug H., Weich H.A.;
"Synthesis and assembly of functionally active human vascular endothelial growth factor homodimers in insect cells.";
Eur. J. Biochem. 211:19-26(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                     Tischer E., Mitchell R., Hartman T., Silva M., Gospodarowicz Fiddes J.C., Abraham J.A.;
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MEDLINE-9477915; Pubmed-9336848;
AEIDINOLPHE W.J., Champe M.A., Christinger H.W., Keyt B.A., Starovasnik M.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Biochem. Biophys. Res. Commun. 183:1167-1174(1992).
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MEDLINE=99119204; PubMed=9922142;
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                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. MEDLINE-91268072; PubMed=1711045;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-92231879; PubMed=1567395; Weindel K., Marme D., Weich H.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 27-41.
MEDLINE=93145946; PubMed=7678805;
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                                                                                                                                                                                                                                                     Science 246:1309-1312(1989)
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                                                                                                           SUBUNIT: HOMODIMER; DISULFIDE-LINKED.
SUBCELLULAR LOCATION: SECRETED BUT REMAINS ASSOCIATED TO CELLS OR
TO THE EXTRACELLULAR MATRIX UNLESS RELEASED BY HEPARIN (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INTERCHAIN.
N-LINKED (GLCNAC. .).
K -> N (IN ISOFORM VEGF-121 AND ISOFORM VEGF-165).
                                 "Solution structure of the heparin-binding domain of vascular endothelial growth factor."; Structure 6:637-64(1998).
-!- FUNCTION: GROWTH FACTOR ACTIVE IN ANGIOCENESIS, AND ENDOTHELIAL CELL GROWTH. INDUCES ENDOTHELIAL PROLIFERATION AND VASCULAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mitogen; Growth factor; Glycoprotein; Alternative splicing; Signal;
                                                                                                                                                              ALTERNATIVE PRODUCTS: FOUR FORMS OF VEGF ARE PRODUCED BY ALTERNATIVE SPLICING OF THE SAME GENE (VEGF-121, VEGF-165, VEGF-189 AND VEGF-215).
SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VASCULAR ENDOTHELIAL GROWTH FACTOR
       Fairbrother W.J., Champe M.A., Christinger H.W., Keyt B.A., Starovasnik M.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MISSING (IN ISOFORM VEGF-165).
MISSING (IN ISOFORM VEGF-121).
7B9759AD5871FF33 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                   JOINED.
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AAA36804.1; JOINED.
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MEDLINE-98298440; PubMed-9634701
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS00249; PDGF_1; 1. PROSITE; PS50278; PDGF_2; 1.
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AAA36804.1;
AAA36804.1;
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ProDom; PD001629; PDGF; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                           AAA36804.1;
CAA44447.1;
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209
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1VPP; 23-FEB-99.
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B40454; B40454.
C40454; C40454.
JQ1463; JQ1464.
JQ1464; JQ1464.
S17348; S17348.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1VGH; 08-APR-98
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142
.215 AA;
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                                                                                                 PERMEABILITY.
                                                                                                                                                 SIMILARITY)
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SIGNAL
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VARSPLIC
SEQUENCE
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EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL;
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ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN HERE) AND A SHORT FORM; ARE PRODUCED BY ALTERNATIVE SPLICING. THE LONG FORM CONTAINS A BASIC INSERT WHICH ACTS AS A CELL REFENTION SIGNAL. DEVELOPMENTAL STAGE: IN KIDNEY EPITHELIAL TISSUES, THE SHORTER BECOME PREDOMINATES IN YOUNG (1 DAY OLD) RATS WHILE THE LONGER FORM BECOMES MORE PREVALANT DURING AGING.

MISCELLANEOUS: A-A AND B-B, AS WELL AS A-B, DIMERS CAN BIND TO THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 58-196 FROM N.A. (SHORT FORM).
STRAINFISCHER 344; TISSUE-Smooth muscle;
STRAINFISCHER 344; TISSUE-Smooth muscle;
Sabo P., Weksler D., Whitington E., Weksler B.B.;
Sabo P., Weksler D., Whitington E., Weksler B.B.;
"The age-dependent proliferation of rat aortic smooth muscle cells is independent of differential splicing of PDGF A-chain mRNA.";
Mech. Ageing Dev. 67:79-89(1993).
-! FUNCTION: PLATELET-DERIVED GROWTH FACTOR IS A POTENT MITGEN FOR CELLS OF MESENCHYMAL ORIGIN. BINDING OF THIS GROWTH FACTOR TO ITS AFFINITY RECEPTOR ELICITS A VARIETY OF CELLULAR RESPONSES. IT IS RELEASED BY PLATELETS UPON WOUNDING AND PLAYS AN IMPORTANT ROLE
                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Increased expression of PDGF A- and B-chain genes in rat lungs with hypoxic pulmonary hypertension."; Am. J. Physiol. 264:L100-L106(1993).
                                               Gaps
                                                                                    25 CTPRNFSVSIREEL-KRTDTIFWPGCLLVKRCGGNCACCLHNCNECQCVPSKVTKKYHEV 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IN STIMULATING ADJACENT CELLS TO GROW AND THEREBY HEAL THE WOUND. SUBUNIT: ANTIPARALLEL DISULFIDE-LINKED DIMER OF NONIDENTICAL (A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
BEDLINE-23191115; Pubmed-8447423;
Katayose D., Ohe M., Yammuchi K., Ogata M., Shirato K., Fujita H.,
Shibahara S., Takishima T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AND B) CHAINS. HOMODIMERS OF A AND B CHAINS ARE IMPLICATED IN TRANSFORMATION PROCESSES.
                                                                                                                                                                                                                                                                                                                                                            01-DEC-1992 (Rel. 24, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
PLATELET-DERIVED GROWTH FACTOR, A CHAIN PRECURSOR (PDGF A-CHAIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Herren B., Weyer K.A., Rouge M., Loetscher P., Pech M.; "Conservation in sequence and affinity of human and rodent PDGF
                                             11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. (SHORT FORM).
Xia Y., Feng L., Tang W.W., Wilson C.B.:
"Cloning and expression of rat platelet-derived growth factor
A-chain.".
    Length 215;
                                             Indels
    DB 1;
  15.7%; Score 104.5; DB 1
27.0%; Pred. No. 0.00071;
ive 21; Mismatches 33
                                                                                                                                                                                                                                                                                                                       204 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ligands and receptors.";
Biochim. Biophys. Acta 1173:294-302(1993).
                                                                                                                                                                       84 LQLRPKTGVRGLHKSLTDVALEHHEECDC 112
                                                                                                                                                                                               107 MRIKPHQG----QHIGEMSFLQHNKCEC 130
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                                                                                                                                                                                                                                                                                                                       PRT;
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                                           24; Conservative
                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rattus norvegicus (Rat).
Query Match
Best Local Similarity
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P28576;
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the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
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INTERCHAIN (BY SIMILARITY).

INTERCHAIN (BY SIMILARITY).

N-LINKED (GLCNAC. . .) (BY SIMILARITY).

GRR -> DVR (IN SHORT ISOFORM).

MISSING (IN SHORT ISOFORM).
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                                                                                                                                                                                                                             PROSITE; PS00249; PDGF_1; 1.
PROSITE; PS50278; PDGF_2; 1.
Glycoprotein; Mitogen; Growth factor; Platelet; Alternative splicing;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25 CTPRNFSVSI-REELKRIDTIF--WPGCLLVKRCGGNCACCLHNCNECQCVPSKV---TK 78
         -! - SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1986 (Rel. 03, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
PLATELET-DERIVED GROWTH FACTOR, A CHAIN PRECURSOR (PDGF A-CHAIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16;
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PLATELET-DERIVED GROWTH FACTOR, A
RECEPTOR BINDING SITE (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                 15.6%; Score 104; DB 1; Length 204; 34.0%; Pred. No. 0.00076; tive 12; Mismatches 34; Indels
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                                       between the Swiss Institute of Bioinformatics and the
                                                                                                                                                                                                                                                                                                                                                                                                            -> T (IN REF. 3).
FA413F74E86F742C CRC64;
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                                                                                                                                                        HSSP, P01127; 1PDG.
InterPro: IPR002400; GF_Cysknot.
InterPro: IPR000072; PDGF.
Pfam: PF00341; PDGF: 1.
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01-NOV-1986 (Rel. 03, Last seq
                                                                                                                                                                                                                                                                                                                                                                                                                     23307 MW;
                                                                                                                                      L06238; AAA41932.1; -. S57864; AAB26134.2; -.
                                                                                                           EMBL; L06894; AAB59693.1; -.
                                                                                                                   CAA78490.1; -. BAA00987.1; -.
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ProDom; PD001629; PDGF; 1.
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204 AA;
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nes 32; Conserv
 PDGF RECEPTOR
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D10106;
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P04085;
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MEDLINE=92283833; PubMed=1317862;
Andersson M., Oestman A., Baeckstroem G., Hellman U.,
Andersson M., Oestman A., Baeckstroem G., Hellman U.,
George-Nascimento C., Westermark B., Heldin C.-H.;
Tassignment of interchain disulfide bonds in platelet-derived growth factor (PDGF) and evidence for agonist activity of monomeric PDGF.";
J. Biol. Chem. 267:11260-11266(1992).
CELLS OF MESENCHYMAL ORIGIN. BINDING OF THIS GROWTH FACTOR FOR CELLS OF MESENCHYMAL ORIGIN. BINDING OF THIS GROWTH FACTOR TO ITS AFFINITY RECEPTOR ELICITS A VARIETY OF CELLULAR RESPONSES. IT IS RELEASED BY PLATELETS UPON WOUNDING AND PLAYS AN IMPORTANT ROLE
CISCURIATE AND ADJACEMENT CELLS TO GROW AND THEREBY HEAL THE WOUND.
CI-SUBUNIT: ANTIPARALLEL DISULFIDE-LINKED DIMER OF NONIDENTICAL (A AND B) CHAINS. HOMODIMERS OF A AND B CHAINS ARE IMPLICATED IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=87287248; PubMed=3614364;
Collins T., Bonthron D.T., Orkin S.H.;
"Alternative RNA splicing affects function of encoded platelet-derived
growth factor A chain.";
Nature 328:621-624(1987).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDINE-86203630; PubMed-3754619;
Betsholtz C., Johnsson A., Heldin C.H., Westermark B., Lind P.,
Urdea M.S., Eddy R., Shows T.B., Philpott K., Mellor A.L., Knott T.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "cDNA sequence and chromosomal localization of human platelet-derived growth factor A-chain and its expression in tumour cell lines."; Nature 320:695-699(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hoppe J., Schumacher L., Eichner W., Weich H.A.; "The Long 3-"untranslated regions of the PDGF-A and -B mRNAs are only distantly related."; FEBS Lett. 223:248-246(1987).
MEDLINE-88144463; PubMed-3422746;
Bonthron D.T., Morton C.C., Orkin S.H., Collins T.;
"Platelet-derived growth factor A chain: gene structure, chromosomal
location, and basis for alternative mRNA splicing.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIINE-93252628; PubMed-8486521;
Takimoto Y., Li W.Y., Wang Z.Y., Tong B.D., Deuel T.F.;
"Nucleotide sequence of the 5' region of the human platelet-derived
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "cDNA clones reveal differences between human glial and endothelial cell platelet-derived growth factor A-chains.";
Nature 328:619-621(1987).
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Tong B.D., Auer D.E., Jaye M., Kaplow J.M., Ricca G., McConathy
Drohan W., Deuel T.F.;
                                                                                                                                                                                                                                                                                             MEDLINE=88174698; PubMed=2832727;
Rorsman F., Bywater M., Knott T.J., Scott J., Betsholtz C.;
"Structural characterization of the human platelet-derived grodistor A-chain cDNA and gene: alternative exon usage predicts different precursor proteins.";
Mol. Cell. Biol. 8:571-577(1988).
                                                                                                                                                                        Proc. Natl. Acad. Sci. U.S.A. 85:1492-1496(1988)
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MEDLINE=88030061; Pubmed=3666150;
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                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS; PRO0438; GFCYSKNOT.
Prodom, PD001629; PDGF; 1.
SMART; SM00141; PDGF; 1.
PROSITE; PS00249; PDGF_1; 1.
PROSITE; PS50278; PDGF_2; 1.
Glycoprotein: Mitogen; Growth factor; Platelet; Alternative splicing; signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PLATELET-DERIVED GROWTH FACTOR, A CHAIN. RECEPTOR BINDING SITE (POTENTIAL).
SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS. DATABASE: NAME=R&D Systems' cytokine source book; WWW="http://www.rndsystems.com/cyt_cat/pdgf.html".
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GRP -> DVR (IN SHORT ISOFORM).
MISSING (IN SHORT ISOFORM).
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48633DDE558EFA43 CRC64;
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EMBL; X03795; CAA27421.1; -.
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Pfam; PF00341; PDGF;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mercola M., Wang C., Kelly J., Brownlee C., Jackson-Grusby L., Stiles C., Bowen-Pope D.; "Selective expression of PDGF A and its receptor during early mouse embryonesis"."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        conservation of gene structure, nucleotide sequence and alternative
                                                                                                                                                                                                                               Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS.
                                                                      01-FEB-1991 (Rel. 17, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
PLATELET-DERIVED GROWTH FACTOR, A CHAIN PRECURSOR (PDGF A-CHAIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rorsman F., Betsholtz C.; "Characterization of the mouse PDGF A-chain gene. Evolutionary
                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. (LONG AND SHORT FORMS)
                              PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    S66874;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     S66871;
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                   PDGA_MOUSE
P20033;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              splicing."
                                                                                                                                                                                 (PDGF-1).
                                                                                                                                                                                                                  PDGFA.
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EMBL;
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EMBL;
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PDGA_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL;
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\$66872;

EMBL;

CKTRTVIXEIPRSQVDFTSANFLIMPPCVEVKRCTG---CC--NTSSVKCQPSRVHHRSV 150 CTPRNFSVSI-REELKRIDTIF--WPGCLLVKRCGGNCACCLHNCNECQCVPSKV---TK 78

15.6%; Score 104; DB 1; Length 211; 34.0%; Pred. No. 0.00079; tive 12; Mismatches 34; Indels

Conservative

Similarity

Query Match Best Local Simi Matches 32;

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SMART;
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                                                                                                                                                                                             SMART; SM00141; PDGF; 1.
PROSITE; PS050249; PDGF_2; 1.
PROSITE; PS50278; PDGF_2; 1.
Glycoprotein; Mitogen; Growth factor; Platelet; Alternative splicing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           34; Indels 16; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25 CTPRNFSVSI-REELKRTDTIF--WPGCLLVKRCGGNCACCLHNCNECQCVPSKV---TK 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=83144004; PubMed=6298772; MEDLINE=83144004; PubMed=6298772; Devare S.G., Reddy E.P., Law J.D., Robbins K.C., Aaronson S.A.; "Nucleotide sequence of the simian sarcoma virus genome: "acclocide sequence of the simian sarcoma virus genome: transforming que product p288is."; Proc. Natl. Acad. Sci. U.S.A. 80:731-735(1983).
-! SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS.
                                                                                                                                                                                                                                                                                                                            REMOVED BY PROTEOLYSIS.
PLATELET-DERIVED GROWTH FACTOR, A
RECEPTOR BINDING SITE (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                     BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
INTERCHAIN (BY SIMILARITY).
INTERCHAIN (BY SIMILARITY).
N-LINKED (GLCNG. . .).
N-RINKED (GLCNG. . .).
N-SING (IN SHORT ISOFORM).
WISSING (IN REF. 1).
V -> I (IN REF. 1).
W; AC4345A10ECF4B39 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15.6%; Score 104; DB 1; Length 211; 34.0%; Pred. No. 0.00079;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Viruses; Retroid viruses; Retroviridae; Gammaretrovirus.
NCBL_TaxID=11817;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TSIS_SMSAV STANDARD; PRT; 226 AA. P01128; 041283; 21-JUL-1986 (Rel. 01, Created) 1-JUL-1986 (Rel. 01, Last sequence update) 15-JUL-1999 (Rel. 38, Last annotation update) PDGF_RELATED TRANSFORMING PROTEIN P28-SIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  79 KYHEVLQLRPKTGVRGLHKSLTDVALEHHEECDC 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Pred. No. 0.00
12; Mismatches
                                     HSSP, P01127; IPDG.
MGD; MGI:97527; Pdgfa.
InterPro; IPR002400; GF_cysknot.
InterPro; IPR000072; PDGF.
Pfam; PF00341; PDGF; P.
PRINTS; PR00438; GFCYSKNOT.
ProDom; PD001629; PDGF; I.
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ΜΣ
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Matches 32; Conservative
EMBL; M29464; AAA39903.1;
                                                                                                                                                                                                                                                                                                                                                  211
162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Simian sarcoma virus.
                        PIR; A37359; A37359.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           211 AA;
                                                                                                                                                                                                                                                                                                                                                                                          DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                        DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VARSPLIC
CONFLICT
CONFLICT
SEQUENCE
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PROPEP
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TSIS_SMSAV
AD POI12S
DT 21-JUL
DT 21-JUL
DT 15-JUL
DE PDGF-R
GN V-SIS.
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OC VITUSE
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RP SEQUEN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 VAEPAMIAECKTRTEVFEIS-RRLIDRINANFLWWPPCVEVQRCSG---CC--NNRNVQC 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Orf virus (strain NZ2) (OV NZ-2).
Viruses; dSDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
Parapoxvirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lyttle D.J., Fraser K.M., Fleming S.B., Mercer A.A., Robinson A.J.; "Homologs of vascular endothelial growth factor are encoded by the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16 LTEEVRLYSCTPRN--FSVSIREELKRTDTIF--WPGCLLVKRCGGNCACCLHNCNECQC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -i- SUBUNIT: HOMODIMER; DISULFIDE-LINKED (BY SIMILARITY).
-i- SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL.
VASCULAR ENDOTHELIAL GROWTH FACTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 226;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            72 VPSKVTKKYHEVLQLRP----KTGV---RGLHKSLTDVALEHHEECDC 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               34; Indels
                                                                                                                                                                                                                                                                                 PROSITE; PS00249; PDGF_1; 1.
PROSITE; PS50278; PGFF_2; 1.
Transforming protein; Oncogene; Growth factor.
SEQUENCE 226 AA; 25411 WW; A16813ABB95B90C5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
VASCULAR ENDOTHELIAL GROWTH FACTOR HOMOLOG PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 15.6%; Score 104; DB 1; Best Local Similarity 33.3%; Pred. No. 0.00084; Matches 36; Conservative 12; Mismatches 34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               poxviruš orf virus."; ..
J. Virol. 68:84-92(1994).
-!- FUNCTION: INDUCES ENDOTHELIAL PROLIFERATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS00249; PDGF_1; 1.
PROSITE; PS50278; PDGF_2; 1.
Mitogen; Growth factor; Glycoprotein; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             133 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HOMOLOG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
EMBL; V01201; CAA24516.1; ALT_INIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=94076465; PubMed=8254780;
                                                             HSSP; P01127; 1PDG.
InterPro; IPR002400; GF_cysknot.
InterPro; IPR000072; PDGF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; S67520; AAB29220.2; -. HSSP; P15692; 1VPF.
                                                                                                                                                       Pfam; PF00341; PDGF; 1.
PRINTS; PR00438; GFCYSKNOT.
ProDom; PD001629; PDGF; 1.
SMART; SM00141; PDGF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR000072; PDGF. Pfam; PF00341; PDGF; 1. ProDom; PD001629; PDGF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
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                                   PIR; A01381; TVMVSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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ID VEGH_ORFN2
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SIGNAL
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VEGFC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                           SEVLKGSECKPRPIVVPVSETHPEL--TSQRFNPPCVTLMRCGG---CC--NDESLECVP 80
                                                                                                                                                                                                                                                                      17 TEEVRLYSCTPRNFSVSIRE---ELKRIDTIFWPGCLLVKRCGGNCACCLHNCNECQCVP 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sharma H.S., Tang Z.H., Gho B.C.H., Verdouw P.D.;
"Nucleotide sequence and expression of the porcine vascular endothelial growth factor."
Biochim. Biophys. Acta 1260:235-238(1995).
-!- FUNCTION: GROWTH FACTOR ACTIVE IN ANGIOGENESIS, AND ENDOTHELIAL CELL GROWTH. INDUCES ENDOTHELIAL PROLIFERATION AND VASCULAR PERMEABILITY (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBUNIT: HOMODIMER; DISULFIDE-LINKED (BY SIMILARITY).
SUBCELLULAR LOCATION: SECRETED BUT REMAINS ASSOCIATED TO CELLS
TO THE EXTRACELLULAR MATRIX UNLESS RELEASED BY HEPARIN (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Euteleostomi;
Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VASCULAR ENDOTHELIAL GROWTH FACTOR. BY SIMILARITY.
                                                                                                       N-LINKED (GLCNAC. . .) (POTENTIAL). 917C0F6883030C39 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 34, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
VASCULAR ENDOTHELIAL GROWTH FACTOR PRECURSOR (VEGF) (VASCULAR
                                                                                                                                                                                            Length 133;
                                                                                                                                                                                                                                  Indels
                                                                 INTERCHAIN (BY SIMILARITY).
INTERCHAIN (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                        SKVTKKYHEVLQLRPKTGVRGLHKSLTDVALEHHEECDCVCRGST 118
                                                                                                                                                                                                                                                                                                                                                                                            TEEVNVSMELLG-ASGSGSNGMQR----LSFVEHKKCDCRPRFTT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chordata; Craniata; Vertebrata;
Cetartiodactyla; Suina; Suidae;
                                                                                                                                                                                     DB 1;
                                                                                                                                                                                                                                    40;
                                                                                                                                                                                       Score 102.5; DB 1 Pred. No. 0.00072;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS00249; PDGF_1; 1.
PROSITE; PS50278; PDGF_2; 1.
Mitogen; Growth factor; Glycoprotein; Signal.
                                                                                                                                                                                                                                    Mismatches
                         SIMILARITY.
SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
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BY
BY
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                                                                                                                                                                                          15.4%;
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114
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14715 N
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                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PERMEABILITY FACTOR)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=9823;
                                                                                                                                                                                                             Similarity
                                                                                                                              AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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CARBOHYD
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P49151;
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                                                                                                                                                                                                                                                                                                                               01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
01-0CT-1996 (Rel. 34, Last annotation update)
20-40G-2001 (Rel. 40, Last annotation update)
VASCULAR ENDOTHELIAL GROWTH FACTOR C PRECURSOR (VEGF-C) (VASCULAR ENDOTHELIAL GROWTH FACTOR RELATED PROTEIN) (VRP) (FLT4 LIGAND) (FLT4-
                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (JUN-1996) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: GROWTH FACTOR ACTIVE IN ANGIGGENESIS, AND ENDOTHELIAL
CELL GROWTH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A., AND SEQUENCE OF 103-120.
MEDLINE-96/178224; PubMed=86/17204;
JOUKOV V., Pajusola K., Kaipainen A., Chilov D., Lahtinen I., Kukk
Saksela O., Kalkkinen N., Alitalo K.;
"A novel vascular endothelial growth factor, VEGF-C, is a ligand for
the Flt4 (VEGFR-3) and KDR (VEGFR-2) receptor tyrosine kinases.";
EMBO J. 15:290-298(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chilov D., Lahtinen I., Kukk
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                                                                                                                                                                                                                                                                                                 CTPRNFSVSIREEL-KRIDTIFWPGCLLVKRCGGNCACCLHNCNECQCVPSKVTKKYHEV
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                                                                                                  (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
Fitz L., Morris J.C., Towler P.S., Long A.J., Greco R.,
Burgess P., Glannotti J., Clarletta A., Hennessey D., Kovacic
Fitzgerald M., Scaltreto H., Weich N., Neben S., Finnerty H.,
Zollner R., Wang J., Nickbarg E., Gassaway R., Turner K.,
                                                                                                                                                                                                Length 190;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIINE-96312526; PubMed-8700872;
Lee J., Gray A., Yuan J., Luoh S.-M., Avraham H., Wood W.I.
"Vascular endothelial growth factor related protein: a ligs
specific activator of the tyrosine kinase receptor F144.",
                                                INTERCHAIN (BY SIMILARITY).
INTERCHAIN (BY SIMILARITY).
N-LINKED (GLCNAC. . ) (POT!
                                                                                                       O4D40B8D7913047F CRC64;
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                                                                                                                                                                                                15.4%; Score 102.5; DB 27.0%; Pred. No. 0.001; tive 20; Mismatches
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  BY SIMILARITY.
BY SIMILARITY.
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Saksela O., Kalkkinen N., Alitalo K.;
EMBO J. 15:1751-1751(1996)
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Mammalia, Eutheria, Primates,
NCBI_TaxID=9606;
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                                                                                                                         22368
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                                                                                                                       190 AA;
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  82
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P49767:
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CARBOHYD
SEQUENCE
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Best Local S:
Matches 24
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use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                POTENTIAL.
VASCULAR ENDOTHELIAL GROWTH FACTOR C.
4 X 24 AA TANDEM REPEATS.
                                                                                                                                                                                                                                                                                                                  4 (PARTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

9F598719DB3E014F CRC64;
                                                                                                                                                                                                    PROSITE; PS00249; PDGF_1; 1.
PROSITE; PS50278; PDGF_2; 1.
Mitogen; Growth factor; Glycoprotein; Signal; Repeat.
                                                                                                                                                                                                                                        POTENTIAL.
                                                                                                                                  InterPro: IPR002400; GF_cysknot.
InterPro: IPR000072; PDGF.
Pfam; PF00341; PDGF; 1.
Probom; PD001629; GFCYSKNOT.
Probom; PM001629; PDGF; 1.
                                                                                                                                                                                                                                                                                                                                                               46883 MW;
                                                                        EMBL; X94216; CAA63907.1;
EMBL; U43142; AAA85214.1;
EMBL; U58111; AAB02909.1;
HASP; P15692; 1VPF.
MIM; 601528;
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419
365
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REPEAT
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Search completed: January 15, 2002, 22:22:37 Job time: 119 sec

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13 LNLLTEEVRLYSCTPRNFSVSIREEL-KRTDTIFWPGCLLVKRCGGNCACCLHNCNECQC 71

0 O O O O

Query Match 15.4%; Score 102.5; DB 1; Length 419; Best Local Similarity 28.2%; Pred. No. 0.0022; Matches 31; Conservative 15; Mismatches 43; Indels 21; Gaps

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January 15, 2002, 22:17:38; Search time 58.55 Seconds (without alignments) 299.790 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                   666
1 AFVFGRKSRVVDLNLLTEEV......DVALEHHEECDCVCRGSTGG 120
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                473505 seqs, 146272329 residues
                                                                                                                                                                                            US-09-457-066-2_COPY_226_345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                             - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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sp_virus:*
sp_vertebrate:*
sp_unclassified:*
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sp_bacteria:*
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Maximum DB seq length: 200000000
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					SUMMARIES	
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Result		Query				
NO.	Score	Match	Match Length DB	DB	ID	Description
1	999	100.0	345	4	Q9UL22	O9u122 homo sapien
2	999	100.0	345	4	Q9NRA1	Q9nral homo sapien
3	624	93.7	345	11	Q9QY71	Q9qy71 mus musculu
4	611	91.7	345	11	O9EQX6	Q9eqx6 rattus norv
5	608	91.3	345	11	Q9JHV8	Q9jhv8 mus musculu
9	585	87.8	345	13	091946	Q9i946 gallus gall
7	324	48.6	290	. 11	Q9D1L8	Q9d118 mus musculu
8	324	48.6	364	4	Q9BWV5	Q9bwv5 homo sapien
σ	324	48.6	370	4	Q9GZP0	O9qzpO homo sapien
10	324	48.6	370	11	Q9EQT1	Ogeqt1 rattus norv
11	180	27.0	34	11	099ЛМ4	Q99jm4 mus musculu
12	121.5	18.2	326	11	035251	035251 rattus norv
13	119.5	17.9	358	11	P97946	P97946 mus musculu
14	115.5	17.3	354	4	043915	043915 homo sapien
15	108.5	16.3	148	13	042571	042571 xenopus lae
16	108.5	16.3	194	13	042572	042572 xenopus lae
17	108	16.2	185	4	Q15354	Q15354 homo sapien
18	108	16.2	226	4	Q9UF23	Q9uf23 homo sapien
19	105.5	15.8	207	4	016528	O16528 homo sapien

Q29613 felis silve Q9bbp7 macaca mula Q9ubB homo sapien Q9ul23 homo sapien Q9ul23 homo sapien Q9ul23 homo sapien Q9ul20 mus musculu Q9ul56 mus musculu Q9usf canis famil Q9xsf3 canis famil Q9xsf4 canis famil Q9xsf5 canis famil Q9xsf5 canis famil Q9xsf5 canis famil Q9xsf6 canis famil Q9xsf7 canis famil Q9xsf7 canis famil Q9xsf8 canis famil Q9xsf8 canis famil Q9xsf9 cours famil Q9xsf9 cours famil Q9xsf8 cours aries Q9mzb1 oris aries	
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1004.5 1004.5 1004.5 1004.5 1004.5 1004.5 1004.5 1002.5 10	
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## ALIGNMENTS

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TISSUE-BRAIN;

XA MEDLINE-2017014; PubMed-10858496;

XA MEDLINE-2017014; PubMed-10858496;

XA MEDLINE-2017004; PubMed-10858496;

XA Hanada T., Ui-Tei K., Miyata Y.;

XI Hanada T., Ui-Tei K., Miyat
                                                                                                                            01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
SECRETORY GROWTH FACTOR-LIKE PROTEIN FALLOTEIN (SPINAL CORD-DERIVED GROWTH FACTOR).
                                                                                                                                                                                                                                                                                                                                                                     Craniata; Vertebrata; Euteleostomi;
Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tsai Y.J., Lee R.K.K., Lin S.P.; "Fallotein, a novel growth factor like gene identified in human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.
                                                                     345 AA
                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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                                                                 Q9UL22
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RESULT
Q9UL22
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SEQUENCE FROM N.A.
TISSUE=OVARY;
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                                                                                                                                                                             61 CCLHNCNECQCVPSKVTKKYHEVLQLRPKTGVRGLHKSLTDVALEHHEECDCVCRGSTGG 120
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                                                 Gaps
                                                                                       1 AFVFGRKSRVVDLNLLTEEVRLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGGNCA 60
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Li X., Ponten A., Aase K., Karlsson L., Abramsson A., Uutela M., Backstrom G., Hellstrom H., Li H., Soriano P., Betsholtz C., Heldin C.-H., Alitalo K., Ostman A., Eriksson U., "PDGF-C is a novel protease-activated ligand for the PDGF alpha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0
                                                 ;
  Length 345;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 666; DB 4; Length 345; 100.0%; Pred. No. 5.7e-68; Live 0; Mismatches 0; Indels
                                                 Indels
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                                                                                                                                                                                                                                                                                                                                                                        01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
PLATELET-DERIVED GROWTH FACTOR C.
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(TrEMBLrel. 13, Last sequence update)
(TrEMBLrel. 17, Last annotation update)
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    Score 666; DB 4;
Pred. No. 5.7e-68;
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PROSITE; PS50278; PDGF_2; 1.
SEQUENCE 345 AA; 39043 MW;
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EMBL, AF244813; AAF80597.1; -.
InterPro; IPR000859; CUB.
InterPro; IPR000072; PDGF.
Pfam; PF00431; CUB; 1.
SMART; SM00042; CUB; 1.
SMART; SM00141; PDGF; 1.
  100.0%;
100.0%;
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Best Local Similarity 100.
Matches 120; Conservative
                                                 Matches 120; Conservative
                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
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Ouery Match
Best Local Similarity
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01-MAY-2000 (
01-JUN-2001 (
FALLOTEIN.
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Q9QY71;
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Q9NRA1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    286 CCLHNCNECQCVPRKYTKKYHEVLQLRPKTGVKGLHKSLTDVALEHHEECDCVCRGNAGG 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Rattus.
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STRAIN-WISTAR; TISSUE-KIDNEY;
Hamada T., Ui-Tei K., Imaki J., Miyata Y.;
"Molecular Cloning of SCDGF-B, a Novel Growth Factor Homologous SCDGF/PDGF-C/fallotein.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
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Tsai Y.-J., Lee R.K.-K., Chen Y.-H., Lin S.-P., Cheng W.T.-K.; "cDNA cloning of fallotein from mouse ovary."; Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases. EMBL, MGD; MGI:1859631; Pdgfc.
InterPro; IPR000859; CUB.
InterPro; IPR000072; PDGF.
                                                                                                                                                                                                                                                                                                                                                        Length 345;
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SMART; SM00042; CUB; 1.
SMART; SM00141; PDGF; 1.
PROSITE; PS01180; CUB; 1.
PROSITE; PS02078; PDGF, 2; 1.
SEQUENCE 345 AA; 38741 MW; 3A58A1F701B84EA2 CRC64;
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
SPINAL CORD-DERIVED GROWTH FACTOR.
                                                                                                                                                                                                                                                                                                                                                   Score 624; DB 11;
Pred. No. 3.5e-63;
8; Mismatches 3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Biochem. Biophys. Res. Commun. 0:0-0(2000)
EMBL. AB033B80; BAB19969.1; -.
InterPro; IPR000859; CUB.
InterPro; IPR000072; PDGF.
Pfam; PF00431; CUB; 1.
SM00442; CUB; 1.
SWMART; SM001442; CUB; 1.
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PROSITE; PS50278; PDGF_2; 1.
SEQUENCE 345 AA; 38734 MW;
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Bukaryota; Metazoa; Chordata;
Mammalia; Butheria; Rodentia;
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                        93.7%;
90.8%;
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Matches 109; Conservative
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Hamada T., Ui-Tei K., Miyata Y.;
Hamada T., Ui-Tei K., Miyata Y.;
"A novel gene derived from developing spinal cords, SCDGF, is a unique member of the PDGF,"YEJF family.";
FEBS Lett. 475:97-102(2000).
EMBL; AB033829; BAB03265.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                              Ding H., Wu X., Kim I., Tam P.P.L., Koh G.Y., Nagy A.;
"The mouse Pdgfc gene: Dynamic expression in embryonic tissues during
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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PROSITE; PS50278; PDGF_2; 1.
SEQUENCE 345 AA; 38886 MW; FA1486BED6D362F8 CRC64;
                                  01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
PLATELET-DERIVED GROWTH FACTOR C.
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
SPINAL CORP-DERIVED GROWTH FACTOR.
                            345 AA
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STRAIN-WHITE LEGHORN; TISSUE-SPINAL CORD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                            PRT;
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EMBL: AF286725; AAF91483.1;

MGD: MGI: 1859631; Pdgfc.

InterPro; IPR0000859; CUB.

InterPro; IPR000072; PDGF.

SMART; SM00042; CUB; 1.
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InterPro; IPR000072; PDGF
                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN-SWISS-WEBSTER/NIH;
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                            PRELIMINARY;
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                                                                                                                           Mus musculus (Mouse).
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Q91946;
                            09JHV8
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Arakawa T., Hara A., Shibata K., Yoshino M., Itoh M., Ishii Y., Arakawa T., Hara A., Shibata K., Yoshino H., Adachi J., Fukuda S., Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., A Aizawa T., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Saito R., Schrim L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., Rasi K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Abronstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Abrons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Norione P., Ring B., Ringwald M., Rodriguez I., Sakamoco N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Whyshaw-Boolis A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S., Wanachioni L., Wanachioni Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                61 CCLHNCNECQCVPSKVTKKYHEVLQLRPKTGVRGLHKSLTDVALEHHEECDCVCRGSTGG 120
                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. NCBL_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hayashizaki Y.; "Functional annotation of a full-length mouse cDNA collection.";
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                                                                                                                87.8%; Score 585; DB 13; Length 345;
85.0%; Pred. No. 1e-58;
iive 11; Mismatches 7; Indels
SMART; SM00141; PDGF; 1.
PROSITE; PS01180; CUB; 1.
PROSITE; PS02028; DDGF_2; 1.
SEQUENCE 345 AA; 38940 MW; 97ACEA992BF5128C CRC64;
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PROSITE; PS50278; PDGF_2; 1.
SEQUENCE 290 AA; 33425 MW; 14214509E6717D4B CRC64;
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Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                          290 AA
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STRAIN-C57BL/6J; TISSUE-EMBRYO;
MEDLINE-21085660; Pubmed-11217851;
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                                                                                                                                                     Matches 102; Conservative
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1110003109RIK.
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Best Local S
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254 RKSK-VDLDRLNDDAKRYSCTPRNYSVNIREELKLANVVFFPRCLLVQRCGGUCGCGTVN 312
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                                                                                                                                                                                                                                                                                                                                                                                                   66 CNECQCVPSKVTKKYHEVLQLRP---KTGVRGLHKSLTDVALEHHEECDCVC 114
                                                                                                                                                                                                                                                                                                                                                                                                                  313 WRSCTCNSGKTVKKYHEVLQFEPGHIKRRGRAKTMALVDIQLDHHERCDCIC 364
                                                                                                                                                                                                                                                                                     Query Match 48.6%; Score 324; DB 4; Length 37 Best Local Similarity 53.6%; Pred. No. 6.6e-29; Matches 60; Conservative 15; Mismatches 33; Indels
                                        "Iris-expressed Growth Factor (IEGF).";
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AB033032; BAB18903.1; ...
EMBL, AF1132116; AAG32287.1; ...
EMBL, AY027517; AAK20081.1; ...
                                                                                                                                                                                        SMART; SMULLE: PSOL180; CUB; 1.
PROSITE; PSOL28; PDGF_2; 1.
PROSITE: PSO0430; TONB_DEPENDENT_REC_1; UNKNOWN_1.
PROSITE: PSO0430; TONB_DEPENDENT_REC_1; UNKNOWN_1.
                                                                                                             InterPro; IPR000859; CUB.
InterPro; IPR000072; PDGF.
InterPro; IPR0000531; TonB_boxC.
Pfam; PF00431; CUB; 1.
SWART; SM00042; CUB; 1.
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SMART: SM0141; PDGF; 1.
PROSITE; PS01180; CUB; 1.
PROSITE; PS0278; PDGF_2;
SEQUENCE 370 AA; 42802)
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  SEQUENCE FROM N.A.
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                 TISSUE-IRIS;
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                              Wistow G.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Liu B., Liu Y.Q., Wang X.Y., Zhao B., Sheng H., Zhao X.W., Liu S., Xu Y.Y., Ye J., Song L., Gao Y., Zhang C.L., Zhang J., Wei Y.J., Cao H.Q., Zhao Y., Liu L.S., Ding J.F., Gao R.L., Wu Q.Y., Qiang B.Q., Yuan J.G., Liew C.C., Zhao M.S., Hui R.T.; Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.
6 RKSRVVDLNLITEEVRLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGGNCACCLHN 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-UNN-2001 (TrEMBLrel. 17, Last annotation update)
SPINAL CORD-DERIVED GROWTH FACTOR-B (MSTP036) (IRIS-EXPRESSED GROWTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
Hamada T., Ui-Tei K., Imaki J., Miyata Y.;
Molecular Cloning of SCDGF-B, a Novel Growth Factor Homologous to SCDGF/PDGF-C/fallotein.".
                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4;
                                        66 CNECQCVPSKVTKKYHEVLQLRP---KTGVRGLHKSLTDVALEHHEECDCVC 114
                                                         233 WKSCTCSSGKTVKKYHEVLKFEPGHFKRRGKAKNMALVDIQLDHHERCDCIC 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     307 WRSCTCNSGKTVKKYHEVLQFEPGHIKRRGRAKTWALVDIQLDHHERCDCIC 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       66 CNECQCVPSKVTKKYHEVLQLRP---KTGVRGLHKSLTDVALEHHEECDCVC 114
                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 364;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      33; Indels
                                                                                                                                                                                                                                                                                                                                                      "Iris-expressed Growth Factor (IEGF).";
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AY027518; AAR, A210682.1; -
SEQUENCE 364 AA; 42166 MW; 245C53EBDDEA9EAC CRC64;
                                                                                                                                            01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
1RIS-EXPRESSED GROWTH FACTOR SHORT FORM.
                                                                                                                                                                                                                                                                                                                                                                                                                                         48.6%; Score 324; DB 4;
53.6%; Pred. No. 6.5e-29;
Live 15; Mismatches 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      60; Conservative
                                                                                                                                         · PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                           Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FACTOR LONG FORM).
HSCDGF-B OR IEGF.
                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                  NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE-AORTA;
                                                                                                                                                                                                                                                                                                                          TISSUE-IRIS;
                                                                                                                                                                                                                                                                                                                                         Wistow G.;
                                                                                                                                         Q9BWV5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9GZP0
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                                                                                                             RESULT
Q9BWV5
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Length 370;

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Eukaryota, Métazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6 RKSRVVDLNLLTEEVRLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGGNCACCLHN 65
                                                                                                                                                                                                                                                                                                                                                                                                                 Hamada T., Ol-Tei K., Imaki J., Miyata Y.;
Hamada T., Ol-Tei K., Imaki J., Miyata Y.;
Hamada T., Ol-Tei K., Imaki J., Miyata Y.;
SCDGF/PORP-C/Fallotein.";
Biochem. Biophys. Res. Commun. 0:0-0(2000).
EMBL; AB052170; BAB18920.1;
InterPro; IPR0000859; CUB.
InterPro; IPR0000929; PDGF.
Pfam; PF00431; CUB; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4 ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JB; 1.
OGF_2; 1.
42809 MW; 7BE8A251F679BF73 CRC64;
                                                                                           01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
SPINAL-CORD DERIVED GROWTH FACTOR-B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match

48.6%; Score 324; DB 11;
Best Local Similarity 52.7%; Pred. No. 6.6e-29;
Matches 59; Conservative 18; Mismatches 31;
                                                             (TrEMBLrel. 16, Created)
PRT;
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Q99JM4; Q99JM4 RESULT 11

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104 LKVIDEEWQRTQCSPRETCVEVASELGKTTNTFFKPPCVNVFRCGG---CC--NEEGVMC 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13 LNLLTEEVRLYSCTPRNFSVSIREEL-KRTDTIFWPGCLLVKRCGGNCACCLHNCNECQC 71
                                                                                                                                                                                                               01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
VASCULAR ENDOTHELIAL GROWTH FACTOR D (C-FOS INDUCED GROWTH FACTOR).
                                                                                                                                                                                                                                                                                      Mus musculus (Mouse).
Sukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Ordandini M., Marconcini L., Ferruzzi R., Oliviero S.; "Identification of a c-fos-induced gene that is related to the platelet-derived growth factor/vascular endothelial growth factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FIGF OR VEGF-D.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Yamada Y., Nezu J., Shimane M., Hirata Y.; "Molecular cloning of a novel vascular endothelial growth factor,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 17.9%; Score 119.5; DB 11; Length Best Local Similarity 33.3%; Pred. No. 1.4e-05; Matches 36; Conservative 15; Mismatches 42; Indels
                                       V---PSKVTKKYHEVLQLRPKTGVRGLHKSLTDVALEHHEECDCVCRG 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               72 V---PSKVTKKYHEVLQLRPKTGVRGLHKSLTDVALEHHEECDCVCRG 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6636B17FBF07037C CRC64;
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Proc. Natl. Acad. Sci. U.S.A. 93:11675-11675(1996)
                                                                                                                                                         358 AA
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                                                                                                                                                         PRT;
                                                                                                                                                                                               Created)
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                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=C57BL/6J;
MEDLINE=97030254; PubMed=8876195;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS00249; PDGF_1; 1.
PROSITE; PS50278; PDGF_2; 1.
SEQUENCE 358 AA; 40908 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL, X99572; CAA67892.1; -.
EMBL, D89628; BAA14002.1; -.
HSSP, P15692; 1VPP.
MGD, MGI:108037; Figf.
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                                                                                                                                                                                             01-MAY-1997 (TrEMBLrel. 03,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR000072; PDGF. Pfam; PF00341; PDGF; 1. ProDom; PD01629; PDGF; 1. SMART; SM00141; PDGF; 1.
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                                                                                                                                                         PRELIMINARY;
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                                                                                                                                                                                                                                                                        VEGF-D OR FIGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FISSUE=LUNG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VEGF-D.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           family.
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P97946
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1D 04
AC 04
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                               01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
SIMILAR TO PLATELET-DERIVED GROWTH FACTOR, C POLYPEPTIDE (FRAGMENT).
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                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Yamada Y., Nezu J., Shimane M., Hirata Y.;
"Molecular cloning of a novel vascular endothelial growth factor,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
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313 WKSCTCSSGKTVKKYHEVLKFEPGHFKRRGKAKNMALVDIQLDHHERCDCIC 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              42; Indels
                                                                                                                                                                                                                                                                                                                                        Strausberg R.;
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC006027; AAH06027.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS00349; PDGF_1; 1.
PROSITE; PS50278; PDGF_2; 1.
SEQUENCE 326 AA; 37112 MW; 1261AFA373596C00 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                        NON_TER 1 1 SEQUENCE 34 AA; 3618 MW; F4AB6A3A414AED9E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ch 18.2%; Score 121.5; DB 1
1 Similarity 33.3%; Pred. No. 7.5e-06;
36; Conservative 15; Mismatches 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 180; DB 11;
Pred. No. 1.6e-13;
2; Mismatches 1
                                                                                               A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     326 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 RPKTGVKGLHKSLTDVALEHHEECDCVCRGNAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Created)
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MEDLINE-97349118; PubMed-9205122;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENOMICS 42:488(1997).
EMBL; AF014827; AAB66557.1; -.
HSSP; P15692; 1VPP.
Interpro; IPRO00072; PDGF.
Pfam; PF00341; PDGF? 1.
ProDom; PD001629; PDGF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27.0%;
ilarity 91.2%;
Conservative
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                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                            TISSUE=MAMMARY TUMOR;
                                                                                                                                                                                                                 Mus musculus (Mouse).
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Best Local Similarity
Matches 31; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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9

Gaps

15;

Matches

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Length 358;

RESULT
035251
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RT Tyrosine kinases VEGF receptor 2 (Flk1) and VEGF receptor 3 (Flt4).";

REMBL; V12864; CAA73371.1; -

REMBL; V12865; CAA73371.1; JOINED.

REMBL; V12866; CAA73371.1; JOINED.

REMBL; V12869; CAA73371.1; JOINED.

REMBL; V12869; CAA73371.1; JOINED.

REMBL; V12869; CAA73371.1; JOINED.

REMBL; V12869; CAA73371.1; JOINED.

REMBL; V12863; CAA73371.1; -

REMBL; V12864; CAA73371.1; -

REMBL; V12864; CAA73371.1; -

REMBL; V12864; CAA73371.1; -

REMBL; V12864; CAA73371.1; -

REMBL; V12864
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                                                                                              MEDLINE=98140120; PubMed=9479493;
Rocchigiani M., Lestingi M., Luddi A., Orlandini M., Franco B.,
Rossi E., Ballabio A., Zuffardi O., Oliviero S.;
"Human FIGF: cloning, gene structure, and mapping to chromosome Xp22.1
between the PIGA and the GRPR genes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE=98118549; PubMed=9435229;
Achen M.G., Jeltsch M., Kukk E., Maekinen T., Vitali A., Wilks A.F.,
Alitalo K., Stacker S.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13 INLITEEVRLYSCTPRNFSVSIREEL-KRTDTIFWPGCLLVKRCGGNCACCLHNCNEC-Q 70
                                                                                                                                                                                                                                                                                                TISSUE-LUNG;
MEDLINE-97349118; PubMed-9205122;
Yamada Y., Nezu J., Shimane M., Hirata Y.;
"Molecular cloning of a novel vascular endothelial growth factor,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Xenopus laevis (African clawed frog).
Sukaryota; Metazota; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 4; Length 354;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                71 CVPSKVTKKYHEVLQLRPKTGVRGLHKSLTDVALEHHEECDCV 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  156 TSTSYISKQLFEISV--PELVPVKVANHTGCKCL 192
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01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
VASCULAR ENDOTHELIAL GROWTH FACTOR 122.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17.3%; Score 115.5; DB 4
33.0%; Pred. No. 3.9e-05;
tive 14; Mismatches 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              148 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS00249; PDGF 1; 1.
PROSITE; PS50278; PDGF 2; 1.
SEQUENCE 354 AA; 40444 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00341; PDGF; 1.
ProDom; PD001629; PDGF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                        Genomics 42:483-488(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR000072; PDGF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SM00141; PDGF; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ouery Match
Best Local Similarity
Matches 34; Conserv
                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                      NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=8355;
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RP SEQUENCE FROM N.A.

RA Cleaver O., Tonissen K.F., Saha M.S., Krieg P.A.;

RL Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases.

DR EMBL; AF008593; AAB63679.1; -..

DR HSSP, P15692; 1VPP.

DR InterPro; IPP000072; PDGF.

DR ProDom; PD00141; PDGF; 1.

DR PROSTTE; SM00141; PDGF; 1.

DR ROSITE; PS50278; PDGF_1.

DR PROSTTE; PS50278; PDGF_2; 1.

SQ SEQUENCE 148 AA; 17234 MW; 4AD153CA2F8B1E95 CRC64;

QUETY Match

QUETY Match

QUETY MATCH

QUETY WATCH

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2 my24b02.rl Barstead 2 602810580F1 NCI\_CGA 4 601810869F1 NTH\_MGC 7 602342635F1 NTH\_MGC 7 PM4-ET0154-15ii.00-0

AA240232 BG914292 BF128614 BG167387 BF876874

'n

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1. :1142
/organism="Homo sapiens"
/organism="Homo sapiens"
/organism="Homo sapiens"
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/clone="InAGE:4752148"
/clone=lib="NuI_CGAP_Sku4"
/tissue=_type="squamous cell carcinoma"
/lab_host="DH108 (T1 phage-resistant)"
/note="Organ: skin; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: Sall; cloned unidirectionally. Primer: Oligo dT.
Site_2: Sall; cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.5kb. Library constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens Sukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 1142) Strimates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 1142) Strimates; Catarrhini; Hominidae; Homo. National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                   BG681390 1142 bp mRNA EST 01-MAY-2001 602627750F1 NCI_CGAP_Skn4 Homo sapiens cDNA clone IMAGE:4752348
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CDNA Library Arrayed by: The 1.W.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLAM10610 row: d column: 13
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Gaps: 0
Percent Identity: 99.167
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520
954
417
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: James Cleaver, M.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         from: 1 to: 1142
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US-09-457-066-2_COPY_226_345 x BG681390
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BG681390
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LOCUS BG681390
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 human.
   gb_estl:AA240232
gb_est2:BG914292
gb_est2:BF128614
gb_est2:BG167387
gb_est2:BF876874
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE
AUTHORS
TITLE
JOURNAL
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | BG185961 RST4916 Athersys RGGE |
| BG185961 RST4916 Athersys RGGE |
| BF021679 Uy50f65.y1 NCI_CGAP_LU |
| BE958470 601644787F1 NIH_MGC_56 |
| BG609411 323221 MARC 1PIG Sus separated in the property of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | AW 67693 | X 1970 |
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                                                                                                                                                                                                                                                                           __MODEL=frame+_p2n_model -DEV=xlh
-Q-Cgn2_1/USPTO_spool/US09457066/runat_15012002_132155_14189/app_query.fasta_1.190
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-Q-Cgn2_1/USPTO_spool/US09457066/runat_15010 -GAPPEXT=4.000
-MINMATCH=0.100 -LOOPCL=0.000 -LOOPEXT=0.000 -FGAPOP=6.000
-FGAPOPT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500 -FGAPOP=6.000
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-ALIGN=15 -MODE=LOCAL -OUTFMT=pfs -NORM=ext -HEAPSIZE=500
-NINLEN=2000000000 -USER=US09457066_QCGN1_L_3596
-NCPU=6 -ICPU=3 -LONGLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Documentation
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6e-06
OM of: US-09-457-066-2_COPY_226_345 to: EST:*
                                                                                                                                               Results were produced by the GenCore Copyright (c) 1993-2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1150.33
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Query: US-09-457-066-2_COPY_226_345
Query length: 120
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Database sequences: 11351937
Database length: 1077921985
Search time (sec): 1201.300000
                                                                               Date: Jan 15, 2002 10:42
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9b_est2:Bd086411

9b_est2:Bd08411

9b_est2:Bd604411

9b_est2:Bd604413

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9b_est2:Bf10865

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9b_est2:Bf10868

9b_est1:Af10869

9b_est1:Bf18889
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gb_est2:BF551964
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gb_est2:BG387377
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                                                                                                                                                  About: Results
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67

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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chordata; Craniata; Vertebrata; Euteleostomi; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomı;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 523)
NCI-CGAP http://www.ncbi.nlm.nih.gov/nciogap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone_lib="NCI_CGAP_Lu30"
/tisbase_rype="tunor, metastatic to mammary"
/lab host="DH10B"
/note="Organ: lung; Vector: pCMV-SPORT6; Site_1: NotI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BF021679 523 bp mRNA EST 29-DEC-2000 uy50f05.yl NCI_CGAP_Lu30 Mus musculus cDNA clone IMAGE:3663009 similar to TR:090Y71 090Y71 FALLOTEIN. ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       367 GCTTTTGTTTTTGGAAGAAAATCCAGAGTGGTGGAGCATCTGAACCTTCTAAC 416
                                                                                                                           67 nGluCysGlnCysValProSerLysValThrLysLysTyrHisGluValL 84
       1 AlaPheValPheGlyArgLysSerArgValValAspLeuAsnLeuTh 17
                                                                                                                                                                                            17 rGluGluValArgLeuTyrSerCysThrProArgAsnPheSerValSerI
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/strain="CZECH II"
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Location/Qualifiers
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/clone="IMAGE:3663009"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Seq primer: -40RP from Gibco
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Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seq_name: gb_est2:BF021679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    house mouse.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                117 rThrGlyGly 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  717 CACAAGAGGA 726
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TITLE
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KEYWORDS
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/db_xref="taxon:9606"
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Libraries using Random Activation of Gene Expression',
Nature Biotechnology, in press. Note that even though the
cell type indicated is HT1080, since a random activation
method was used, these sequence tags are not necessarily
expressed in HT1080 under normal circumstances."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 811)
Harrington, J.J., Sherf, B., Rundlett, S., Jackson, P.D., Perry, R., Cain, S., Dahl, T., Thornton, M., Ramachandran, R., Whittington, J., Lerner, L., Krashoc, D., McElligott, K., Clark, S., Mays, R., Smith, E., Veloso, N., Hess, J., Cothren, K., Lo, K., Offenbacher, J., Danzig, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Creation of Genome-wide Protein Expression Libraries using Random
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        seq_documentation_block:
LOCUS BG185961 811 bp mRNA EST 21-APR-2001
DEFINITION RST4916 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.
ACCESSION BG1865961 GI:13707648
euGlnLeuArgProLysThrGlyValArgGlyLeuHisLysSerLeuThr 100
                                                                                                                                                                                                                       522
                                                                                                                                                                                                                                                                 101 AspValAlaLeuGluHisHisGluGluCysAspCysValCysArgGlySe 117
                                                                                                                                                                                                                                                                                             nGluCysGlnCysValProSerLysValThrLysLysTyrHisGluValL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Activation of Gene Expression
Nat. Biotechnol. 19 (5), 440 (2001) In press
Contact: Scott J. Cain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Athersys, Inc.
3201 carnegie Ave, Cleveland, OH 44115, USA
TE1: 216 431 9900
Tex: 216 361 9596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps: 0
Percent Identity: 98.333
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Location/Qualifiers
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US-09-457-066-2_COPY_226_345 x BG185961
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Ratio:
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ORGANISM

REFERENCE AUTHORS JOURNAL

COMMENT

TITLE

FEATURES

VERSION KEYWORDS SOURCE

117

Align seg 1/1

BASE COUNT

ORIGIN

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/clone_lhe_NINIH_MGC_56"
/clone_lhe_NINIH_MGC_56"
/tissue_type="primitive neuroectoderm"
/lab_host="bullob (Ti phage-resistant).
/note="lorgan: brain: Vector: pDNR-LiB (Clontech); Site_1:
Sfil (ggccgctcggcc); Site_2: Sfil (ggccattatggcc);
Double-stranded cDNA was prepared from cell line RNA. 5'
and 3' adaptors were used in cloning as follows: 5'
adaptor sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor
sequence: 5'-ATTCTAGAGGCCGACGATC-4T(30)BN-3'
(where B = A, C, or G and N = A, C, G, or T). Average
insert size 1.65 kb (range 0.9-4.0 kb). 15/15 colonies
contained inserts by PCR. This library was enriched for
full-length clones and was constructed by Clontech
Laboratories (Palo Alto, CA)."
129 q 128 t
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov.
Plate: LLCM/63 row: m column: 22
High quality sequence start: 2
High quality sequence stop: 513.
Location/Qualifiers
1. 523
//Ar sortion/Qualifiers
1. 524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      201 AGAGGAGGTAAGATTATACAGCTGCACACCTCGTAACTTCTCAGTGTCCA 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AspValAlaLeuGluHisHisGluGluCysAspCysValCysArgGlySe 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 AlaPheValPheGlyArgLysSerArgValValAspLeuAsnLeuLeuTh 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    34 leArgGluGluLeuLysArgThrAspThrIlePheTrpProGlyCysLeu 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  rGluGluValArgLeuTyrSerCysThrProArgAsnPheSerValSerI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    51 LeuValLysArgCysGlyGlyAsnCysAlaCysCysLeuHisAsnCysAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length: 120
Gaps: 0
Percent Identity: 98.333
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           alignment_block:
US-09-457-066-2_COPY_226_345 x BE958470
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5.254
98.333
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ratio
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                                                                                                                                                         source
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                                                                                                                                   FEATURES
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 523)
National Institutes of Health, Mammalian Gene Collection (MGC)
National Institutes of Health, Mammalian Gene Collection (MGC)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nh.gov
Tissue Procurement: ATCC
cDNA Library Preparation: CLONETECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
  Site_2: Sall; transgenic model WNT-1, expression driven by MMTV-LTR enhancer: Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies.
Investigator providing samples: Gilbert Smith, NIH"
116 c 139 g 125 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seq_documentation_block:
LOCUS BE958470 523 bp mRNA EST 04-OCT-2000
DEFINITION 601644787F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:3930045
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   euGlnLeuArgProLysThrGlyValArgGlyLeuHisLysSerLeuThr 100
                                                                                                                                                                                                                                                                                                                                                                                                        314 CTGGTCAAGCGCTGTGGAGGAAATTGTGCCTGTTGTCTCCATAATTGCAA 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              101 AspValAlaLeuGluHisHisGluGluCysAspCysValCysArgGlySe 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LeuvalLysArgCysGlyGlyAsnCysAlaCysCysLeuHisAsnCysAs 67
                                                                                                                                                                                                                                                                                                                                                                                     1 AlaPheValPheGlyArgLysSerArgValValAspLeuAsnLeuLeuTh 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           nGluCysGlnCysValProSerLysValThrLysLysTyrHisGluValL 84
                                                                                                                                                                                           Length: 120
Gaps: 0
Percent Identity: 90.833
                                                                                                                                                                                                                                                                                                                                            from: 1 to: 523
                                                                                                                                                                                                                                                                             alignment_block:
US-09-457-066-2_COPY_226_345 x BF021679
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BE958470
BE958470.1 GI:10569175
                                                                                                                                                                                           624.00
5.288
98.333
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                                                                                                                                                                                             Quality:
Ratio:
                                                                                                                                                                                                                                  Percent Similarity:
                                                                                        143
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                                                                                      BASE COUNT
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                                                                                                           ORIGIN
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/ Organism="Homo sapiens"
/ Ob xref="taxon:9666" |
/ Clone="IMAGE:4750095" |
/ Clone="IMAGE:4750095" |
/ Clone="Lib="NoI_CGAP_Skn4" |
/ Clisue_type="squamous cell carcinoma" |
/ Lab_host="DH10B (TI phage-resistant) |
/ Tab_host="Cloned unidirectionally |
/ Site_2: Sal; Cloned unidirectionally |
/ Primer: Oligo dT.
/ Average insert size | 1.5kb | Library constructed by Life |
/ Technologies: Note: this is a NCI_CGAP Library."
                                                                                                                                                                                                                                                            seq_documentation_block:
LOCUS BG677432 969 bp mRNA EST 01-MAY-2001
DEFINITION 602625259F1 NCI_CGAP_SKn4 Homo sapiens cDNA clone IMAGE:4750095 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryotani Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. I (bases 1 to 969)
NIH-WGC http://mgc.nci.nih.gov/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: cgapbs-remail.nih.gov
Tissue Procurement: James Cleaver, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrapa by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
  415 TGAGTGTCAGTGTCCCCCAGCAAAGTCACCAAGAAATATCACGAGGTCC 464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10 ValValAspLeuAsnLeuLeuThrGluGluValArgLeuTyrSerCysTh 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          43 hrIlePheTrpProGlyCysLeuLeuValLysArgCysGlyGlyAsnCys 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLAM10604 row: f column: 16
High quality sequence stop: 764.
Location/Qualifiers
                                           4 GTGGTGGATCTGAACCTTCTAACAGAGGAGGTAAGATTATACAGCTGCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps: 0
Percent Identity: 99.099
                                                                                                                               Length:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   alignment_block:
US-09-457-066-2_COPY_226_345 x BG677432
                                                                                                                                                                                                                                                                                                                                                                                  BG677432.1 GI:13908829
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ratio: 5.559
Percent Similarity: 100.000
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BG677432
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TITLE
JOURNAL
COMMENT
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                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus. 1 (bases I to 556) Fahrenkrug, S.C., Freking, B.A., Rohrer, G.A., Smith, T.P.L., Casas, E., Stone, R.T., Heaton, M.P., Grosse, W.M., Bennett, G.A., Laegreid, W.W. and Keele, J.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Single pass sequencing. Bases called and alt_trimmed with phred vo.380904.4. Vector identified by cross_match with the 'minscore 18 and 'minmatch 12 options.
PCR PRimers
                                                                                                                                                                                                                                                                                                         Design and use of two pooled tissue normalized cDNA libraries for EST discovery in swine Unpublished (2000)
Contact: Smith TPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="Vector: pCMV SPORT6; Site_1: XbaI; Site_2: XhoI; Library made from pooled tissue from day 11, 13, 15, 20, and 30 embryos."
                         17-APR-2001
               BG609411 556 bp mRNA EST 1.
323251 MARC 1PIG Sus scrofa cDNA 5', mRNA sequence.
BG609411
BG609411.1 GI:13659390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        265 AGAAGAAGTGAGGCTATACAGCTGCACCCTAGGAACTTTTCAGTGTCTA 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             34 leArgGluGluLeuLysArgThrAspThrIlePheTrpProGlyCysLeu 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           51 LeuValLysArgCysGlyGlyAsnCysAlaCysCysLeuHisAsnCysAs 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               67 nGluCysGlnCysValProSerLysValThrLysLysTyrHisGluValL 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17 rGluGluValArgLeuTyrSerCysThrProArgAsnPheSerValSerI
                                                                                                                                                                                                                                                                                                                                                                                              USDA, ARS, US Meat Animal Research Center PO Box 166, Clay Center, NE 68933-0166, USA Tel: 402 762 4366 Fax: 402 762 4390 Email: smith@email.marc.usda.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps: 0
Percent Identity: 97.368
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Sus scrofa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone_lib="MARC lPIG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Seg primer: ATTTAGGTGACACTATAG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="taxon:9823"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /tissue_type="pooled"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FORWARD: AGGAAACAGCTATGACCAT
BACKWARD: GTTTTCCCAGTCACGACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
1. .556
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US-09-457-066-2_COPY_226_345 x BG609411
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5.487
99.123
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seq_documentation_block:
                                                                                                                                      pig.
Sus scrofa
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                                           DEFINITION
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FEATURES

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from: 1 to:

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alignment_block:
US-09-457-066-2_COPY_226_345 x BF151355
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COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: Sall; Site_2: Not1; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigators providing samples: Lothar Hennighausen/Robin Humphreys,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. I to Sasa I t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     uzī5b12.y1 NCI_CGAP_Mam5 Mus musculus cDNA clone IMAGE:3669119 5'similar to TR:090y71 090Y71 FALLOTEIN. ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29-DEC-2000
                                                                                                                                                                                                                                                                                           204 TACTAAAAAATACCACGAGGTCCTTCAGTTGAGACCAAAGACGGGTGTCA 253
                                                                                                                               154 GCCTGTTGTCTCCACAATTGCAATGTCAATGTCAATGTCCCAAGCAAAGT 203
                                                                                                                                                                                                                                                                                                                                                                                                         93 rgGlyLeuHisLysSerLeuThrAspValAlaLeuGluHisHisGluGlu 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                      254 GGGGATTGCACAAAATCACTCACCGACGTGGCCCTGGAGCACCATGAGGAG 303
    104 ccarrrrcresccassrrsrcrcresrraaacscressrssaacrer 153
                                                                                      16
                                                                                                                                                                                                                                             76 lThrLysLysTyrHisGluValLeuGlnLeuArgProLysThrGlyValA 93
                                                                                  60 AlaCysCysLeuHisAsnCysAsnGluCysGlnCysValProSerLysVa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone="IMAGE:3669119"
/clone_lib="NCI_CGAP_Mam5"
/tissue_type="tumor, gross tissue"
/dev_stage="7 months"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps: 0
Percent Identity: 88.889
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1. .564
/organism="Mus musculus"
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High quality sequence stop: 436.
Location/Qualifiers
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/db_xref="taxon:10090"
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Percent Similarity: 96.581
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LOCUS BF151355
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KEYWORDS
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Research Center (DKF2); Email S.wiemann@dKf2- heidelberg.de; sequenced by MediGenomix (Martinsried/Germany) within the cDNA sequencing consortium of the German Genome Project. No sl sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Am Klopferspitz 18a D-82152 Martinsried, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Berlin.
6, 14059
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This clone (DKFZp586J0421) is available at the R2PD in Please contact the R2PD: Ressourcenzentrum, Heubnerweg Berlin- Charlottenburg, GERMANY; Email: clone@rzpd.de. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                211 GCTTTCCTGTATGGGAAAAAAGCAAAGTGGTGAATCTGAATCTCCCTCAA 260
                                                                                                                                         261 GGAAGAGGTAAAACTCTACAGCTGCACACCCCGGAACTTCTCAGTGTCCA 310
                                                                                                                                                                                                                                                        euGlnLeuArgProLysThrGlyValArgGlyLeuHisLysSerLeuThr 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         101 AspValAlaLeuGluHisHisGluGluCysAspCysValCysArgGlySe 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     511 GATGTGGCTCTTGAACACCACGAGGAATGTGACTGGGTGTGAGGGGA 560
                                                                                                            34
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1 AlaPheValPheGlyArgLysSerArgValValAspLeuAsnLeuTh 17
                                                                                                            17 rGluGluValArgLeuTyrSerCysThrProArgAsnPheSerValSerI
                                                                                                                                                                                                                         34 leArgGluGluLeuLysArgThrAspThrIlePheTrpProGlyCysLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                               67 nGluCysGlnCysValProSerLysValThrLysLysTyrHisGluValL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="DKFZp586J0421"
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Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Ottenwaelder B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AL047637.1 GI:4728633
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column: 19

us-09-457-066-2\_copy\_226\_345.rst

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Plate: LLAM10323
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                                                      source
                                                                                                                                                                                                                                                                             COUNT
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KEYWORDS
SOURCE
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                                   FEATURES
                                                                                                                                                                                                                                                                             BASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BG243001 910 bp mRNA EST 13-FEB-2001 602355974F1 NCI_CGAP_Mam1 Mus musculus cDNA clone IMAGE:4483938 5',
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Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
1 (bases 1 to 910)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                  /note="Vector: pSport1; Site_1: NotI; Site_2: SalI/MluI"
68 c 80 g 70 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs.rémail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      101
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                                                                                                                                                                                                                                                                                                                                                                                             2 GAGGAGGTAAGATTATACAGCTGCACACCTCGTAACTTCTCAGTGTCCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GluCysGlnCysValProSerLysValThrLysLysTyrHisGluValLe
                                                                                                                                                                                                                                                                                                                            18 GluGluValArgLeuTyrSerCysThrProArgAsnPheSerValSerIl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      152 GAATGTCAATGTCCCCAAGCAAAGTTACTAAAAAATACCACGAGGTCCT
                                                                                                                                                                        101
                                                                                                                                                                                                          Percent Identity: 99.010
/clone_lib="586 (synonym: hutel)"
/tissue_type="uterus"
/dev_stage="adult"
/lab_host="DH10B"
                                                                                                                                                                        Length:
                                                                                                                                                                                            Gaps:
                                                                                                                                                                                                                                         alignment_block:
US-09-457-066-2_COPY_226_345 x AL047637
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BG243001
BG243001.1 GI:12752725
                                                                                                                                                                                      Ratio: 5.624
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                           to: AL047637
                                                                                                                                                                        568.00
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LOCUS BG243001
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                                                                                                                                                                        Quality:
Ratio:
                                                                                                                                                        alignment_scores
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                                                                                                                                                                                                                                                                                           Align seg 1/1
                                                                                  BASE COUNT
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VERSION
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AUTHORS
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SOURCE
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                                                                                                     ORIGIN
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/close_lib="NCI_CGAP_Mam1"
/dv.sue_type="tumor, biopsy sample"
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/lab_lost="DH108"
/note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: SalI;
/note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: SalI;
/ibb_rary constructed by Life Technologies. Investigator
providing samples: glibert Smith, NIH"
/ 220 c 250 g 198 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       seq_documentation_block:
LOCUS BF102859 851 bp mRNA EST 19-OCT-2000
DEFINITION 601646827F1 NIH_MGC_60 Homo sapiens cDNa clone IMAGE:4073095 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               101 AspValAlaLeuGluHisHisGluGluCysAspCysValCysArgGlySe 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           51 LeuValLysArgCysGlyGlyAsnCysAlaCysCysLeuHisAsnCysAs 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       nGluCysGlnCysValProSerLysValThrLysLysTyrHisGluValL 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17 rGluGluValArgLeuTyrSerCysThrProArgAsnPheSerValSerI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      205 GGAAGAGGTAAAACTCTACAGCTGCACACCCGGGAACTTCTCAGTGTCCA
                                                                                                                                                                                                                                                                                                                                                                                                            Length: 120
Gaps: 0
Percent Identity: 90.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    to: BG243001 from: 1 to: 910
                                                                            /organism="Mus musculus"
                                                                                              /strain="FVB/N"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      alignment_block:
US-09-457-066-2_COPY_226_345 x BG243001
row: d
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BF102859.1 GI:10885385
                                                                                                                                                                                                                                                                                                                                                                                                                                4.838
                                                                                                                                                                                                                                                                                                                                                                                                              566.00
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503 CGCAGGAGGG 512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         117 rThrGlyGly 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                  Ratio:
                                                                                                                                                                                                                                                                                                                242
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                                                                                                                                                                                                                                                                                                                                                                                              alignment_scores:
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453 GACCAAAGACCGGTGTCAGGGGATG.CACAAATCACTCACCGACGTG... 498

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 851)
                                                                                                                                                                                DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.W.A.G.E. Consortium/I.LNL at:
http://image.llnl.gov.f column: 08
                                                 NIH MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                    cDNA Library Preparation: CLONETECH Laboratories, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      87 rgProLysThrGlyValArgClyLeuHisLysSerLeuThrAspValAla 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     70 nCysValProSerLysValThrLysLysTyrHisGluValLeuGlnLeuA 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4 PheGlyArgLysSerArgValValAspLeuAsnLeuLeuThrGluGluVa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20 lArgLeuTyrSerCysThrProArgAsnPheSerValSerIleArgGluG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   37 luLeuLysArgThrAspThrIlePheTrpProGlyCysLeuLeuValLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    54 ArgCysGlyGlyAsnCysAlaCysCysLeuHisAsnCysAsnGluCysGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     204 TITGGAAGAAATCCAGAGTGGTGGATCTGAACCTTCTAACAGAGGAGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length: 118
Gaps: 2
Percent Identity: 94.915
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     210 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Align seg 1/1 to: BF102859 from: 1 to: 851
                                                                                 Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-457-066-2_COPY_226_345 x BF102859
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169 c
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96.610
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Ratio:
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COMMENT
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/tissue_rype="hypernephroma"
/lab_host="hypernephroma"
/lab_host="hypernephroma"
/lab_host="ngdan right" vector: pDNR-LiB (clontech); Site_1:
Sfil (ggcgctctggcc); Site_2: Sfil (ggccattatggcc);
Stil (ggcgctctggcc); Site_2: Sfil (ggccattatggcc);
Double-stranded cDNA was prepared from cell line RNA. 5'
and 3' adaptors were used in cloning as follows: 5'
adaptors sequence: 5'-ATCTAGAGCGAGGGGGCGCATAGGGCC3' and 3' adaptor
sequence: 5'-ATTTAGAGGCGAGGGGGGGGGGGATGGTI) Average
insert size 1:35 kb (range 0.94.0 kb). 15/15 colonies
contained inserts by PCR. This library was enriched for.
full-length clones and was constructed by Clontech
Laboratories (Palo Alto, CA)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia; Eutheria, Primates, Catarrhini, Hominidae, Homo. I (bases 1 to 950)
NIH-WGC http://mgc.nci.nih.gov/.
                                                                                                                                                                                                                                         seq_documentation_block:
LOCUS BF031624 950 bp mRNA EST 10-OCT-2000
DEFINITION 601558104F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3827760 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CDNA Library Preparation: CLONETECH Laboratories, Inc.
CDNA Library Preparation: CLONETECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM497 row: h column: 01
High quality sequence stop: 415.
Location/Qualifiers
1. 950
499 GCCTGAGCACCATGAGGAGTGTGACTGTGTGCGAGGGAGCCACAGGGG 548
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Gaps: 0
Percent Identity: 97.895
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
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/clone="IMAGE:3827760"
/clone_lib="NIH_MGC_58"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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US-09-457-066-2_COPY_226_345 x BF031624
                                                                                                                                                                                                                                                                                                                  mRNA sequence.
BF031624
BF031624.1 GI:10739336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5.564
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TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                            ACCESSION
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3 ACACCTCGTAACTTCTCAGTGTCCATAAGGGAAGAACTAAAGAGAACCGA

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seq_name: gb_est2:BF670092
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LOCUS
BF670092
                                                  Quality:
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Percent Similarity:
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                          alignment_scores:
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ORGANISM
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AUTHORS
TITLE
JOURNAL
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DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LINL at:
image.llnl.gov/image/html/iresources.shtml
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="Vector: pryTab-Pac (Pharmacia) with a modified polylinker; Site_1: NotI: Site_2: EcoRI: 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' Taranded with a Not I - oligo(dT) primer [5' Taranded CDNA was ligated to Eco RI adaptors 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pr773 vector. Library constructed and normalized by Bento Soares and M.Fatima
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: cgapbs-r@mail.nih.gov
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 447)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 us37d10.yl Soares_NMEBA_branchial_arch Mus musculus cONA clone
IMAGE:3169267 5' similar to TR:090y71 090y71 FALLOTEIN. ;, mRNA
                                                                                                                    103 GTGCCTGTCCTCTCCACAATTGCAATGTAATGTCAATGTCCCAAGCAAA 152
                                                                                                                                                                                                                                                                                                            203 CAGGGGATTGCACAAAATCACTCACCGACGTGGCCCTGGAGCACTATGAGG 252
                                              102
                                                                                                                                                                                                                                                                                  92 lArgGlyLeuHisLysSerLeuThrAspValAlaLeuGluHisHisGluG 109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone_lib="Soares NMEBA_branchial_arch"
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                        42 pThrIlePheTrpProGlyCysLeuLeuValLysArgCysGlyGlyAsnC
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                                                                                                                                                                                        76 ValThrLysLysTyrHisGluValLeuGlnLeuArgProLysThrGlyVa
                                                                                                                                                                                                                                                                                                                                                                              109 luCysAspCysValCysArgGlySerThrGlyGly 120
                                                                                                                                                                                                                                                                                                                                                                                                        253 AGTGTGACTGTGTGCAGAGGGAGCACAGGAGGA 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Mus musculus"
/db_xref="taxon:10090"
/clone="IMAGE:3169267"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mRNA
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BF011835.1 GI:10712110
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104 c
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LOCUS
BF011835
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KEYWORDS
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109

108 9

126

BASE COUNT

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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 (bases 1 to 874)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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Clone distribution: MGC clone distribution information can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100
                                                                                                                                                                                                                  348 TGAATGTCAGTGTCCCACGTAAAGTTACAAAAAGTACCATGAGGTCC 397
                                                                                                                                                                                                                                                                                                                               198 GGAAGAGGTAAAACTCTACAGCTGCACACCCCGGAACTTCTCAGTGTCCA 247
                                                                                                                                                                                                                                                                                                                                                                                                                   248 TACGGGAAGAGCTAAAGAGGACAGATACCATATTCTGGCCAGGTTGTCTC 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         298 CIGGICAAGCGCIGIGGAGGAAATIGIGCCIGIIGICICCCAIAATIGCAA 347
                                                                                                                                                                                                                                                                                      34
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                                                                                                                                                                                                1 AlaPheValPheGlyArgLysSerArgValValAspLeuAsnLeuLeuTh 17
                                                                                                                                                                                                                                                                                                                                                                        34 leargGluGluLeuLysargThraspThrIlePheTrpProGlyCysLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                              found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLCM1097 row: a column: 06
High quality sequence stop: 598.
                                                                                                                                                                                                                                                                                      rGluGluValArgLeuTyrSerCysThrProArgAsnPheSerValSerI
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/tissue_type="primitive neuroectoderm"
/lab_host="DH10B (T1 phage-resistant)"
                                                                                                                                                                                                                                                                                                          Percent Identity: 91.000
                      Gaps:
Length:
                                                                                                                                                   from: 1 to: 447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
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                                                                                 alignment_block:
US-09-457-066-2_COPY_226_345 x BF011835
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                  5.245 98.000
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Unpublished (1999)
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                                                                                                                                                                                                                                                                  source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BASE COUNT
       JOURNAL
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                                                                                                                                                                                                                                               FEATURES
                        COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORIGIN
/note="Organ: brain; Vector: pDNR-LIB (Clontech); Site_1: Sfil (ggccgctcggcc); Site_2: Sfil (ggccattatggcc); Double-stranded cDNA was prepared from cell line RNA. 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence: 5'-ATTCTAGAGCCGAGCGCGCATG-TGTB) N-3' (where B = A, C, or G and N = A, C, Or T). Average insert size 1.65 kb (range 0.9-4.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Euteleostomi;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                seq_documentation_block:
LOCUS BG118707 968 bp mRNA EST 30-JAN-2001
DEFINITION 602348280F1 NIH_MGC_90 Homo sapiens cDNA clone IMAGE:4443498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 103 AlaLeuGluHis.HisGlu.GluCysAspCys.ValCysArgGlySerTh 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  377 GCCCTGGAGCACGATGAGAGAGAGAGAGAGGAGCAC 426
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21 gLeu..TyrSerCysThrProArgAsnPheSerValSerIleArg.GluG 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5 GlyArgLysSerArgValValAspLeuAsnLeuLeuThrGluGluValAr 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length: 122
Gaps: 8
Percent Identity: 86.885
                                                                                                                                                                                                                                                                                                                                                                                                                                 from: 1 to: 874
                                                                                                                                                                                                                                                                                                                                                                         alignment_block:
US-09-457-066-2_COPY_226_345 x BF670092
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BG118707
BG118707.1 GI:12612213
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                                                                                                                                                                                                                                                                                                                                       Percent Similarity:
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Ratio:
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                                                                                                                                                                                                         BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACCESSION
VERSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KEYWORDS
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/tissue_type="adenocarcinoma, cell line"

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/tab_host="UniUni phage-resistant"

/note="Organ: liver; Vector: pcMv-SPORT6; Site_1: Not1; Site_2: Sal1; Cloned unidirectionally; oligo-dT primed. Average insert size 1.7 kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NIH_MGC Library."

a 230 c 219 g 206 t
                                                                             cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The L.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    288
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     289 GTTAAACGCTGTGGTGGGAACTGTGCCTGTTGTCTCCACAATTGCAATGA 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 PheValPheGlyArqLysSerArqValValAspLeuAsnLeuLeuThrGl 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18 uGluValArgLeuTyrSerCysThrProArgAsnPheSerValSerIleA 35
                                                                                                                                                                         found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLAM10217 row: o column: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    35 rgGluGluLeuLysArgThrAspThrIlePheTrpProGlyCysLeuLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     277 ......GGTTGTCTCCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 52 ValLysArgCysGlyGlyAsnCysAlaCysCysLeuHisAsnCysAsnGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   274 GGA.....
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Percent Identity: 76.471
                                                                                                                                                                                                                                                    High quality sequence start: 8
High quality sequence stop: 574.
Location/Qualifiers
1. 968
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   from: 1 to: 968
       Ph.D.
Contact: Robert Strausberg, F
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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US-09-457-066-2_COPY_226_345 x BG118707
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seq_document LOCUS DEFINITION	ck: 877 nigrovix	
ACCESSION VERSION KEYWORDS SOURCE ORGANISM	odon nigroviridis, genomic survey caniata; Vertebrata; Buteleostomi	
REFERENCE	stei; Neoteleos raodontiformes	
AUTHORS	izames, W., Ber	
JOURNAL REFERENCE AUTHORS	, de	
TITLE	Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F., Saurin, W. and Weissenbach, J. Human gene number estimate provided by genome wide analysis using	
JOURNAL REFERENCE		
AUTHORS TITLE JOURNAL COMMENT	Genoscope.  Direct Submission  Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis	
FEATURES	<pre>yenome. ror more information, prease take a fook at http://www.genoscope.cns.fr/Tetraodon. Location/Qualifiers 1 977</pre>	
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30 ese           607 CTC	eSerValSerIleArgGluGluLeuLysArgThrAspThrIlePheTrpP 47 	
47 rog   :   557 CAA	rodlycysLeuLeuValLysArgcysGlyglyAsncysAlacysCysLeu 63    :::	
64 His	HisAsnCysAsnGluCysGlnCysValProSerLysValThrLysLysTy	

	CysAspCysValCysArg 115 	110
28	::      :::	107
109		. 93
108	TGTCCAACAATGTTGTCAGGTTCTGCTGAAACATGGTGGCA	157
63		83
158	7 TAAATGGCATTTGATCGATAATATGATCACGTTTAAGATGAAATGTTTGA	207
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208	7 CTGCAATATTTGTTTTAATACAAACAAAATCAACAAATCAAAGACCAAGC	257
82		82
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82		82
308	7 GCTGTTGCCATTACACAATACTACAATKCCAGACACTGTGAAATGTACAA	357
82		82
358	7 CTGCCCTTTTAAAAGATTTTGAAATGCGCGGTTGGAACCTTCACAATTTT	407
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408		457
82		80
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